



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 123592

**TO: Gerald G Leffers**

**Location: REM/2A69/2C70**

**Art Unit: 1636**

**Thursday, June 03, 2004**

**Case Serial Number: 09/769699**

**From: Alex Waclawiw**

**Location: Biotech-Chem Library**

**Rem 1A71**

**Phone: 272-2534**

**[Alexandra.waclawiw@uspto.gov](mailto:Alexandra.waclawiw@uspto.gov)**

### Search Notes

From: Leffers, Gerald  
 Sent: Wednesday, June 02, 2004 2:59 PM  
 To: STIC-Biotech/ChemLib; Yucel, Irem  
 Subject: RE: 09/769,699

~~Can anyone give me a status update for this search? This is an After-Final case that has a fairly tight deadline on it. It would be very useful to be able to allow the claims if they are in fact free of any of the more recently issued patents and/or pending applications. Thank you for your help. Gerry Leffers~~

*Gerald G. Leffers Jr., PhD*  
 Primary Examiner, Art Unit 1636  
 Remsen Building, Room 02A69  
 (571) 272-0772

-----Original Message-----

From: Fredman, Jeffrey  
 Sent: Thursday, May 20, 2004 9:39 AM  
 To: STIC-Biotech/ChemLib  
 Cc: Leffers, Gerald  
 Subject: FW: 09/769,699

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Leffers, Gerald  
 Sent: Thursday, May 20, 2004 8:01 AM  
 To: Fredman, Jeffrey  
 Subject: 09/769,699

Hi Jeff, please approve a RUSH updated search of issued and pending files for SEQ ID NO: 2 of this application (~ 1,200 amino acid residues). This is an After-Final that may well be allowable. As always, thank you for your help.  
 Gerry

*Gerald G. Leffers Jr., PhD*  
 Primary Examiner, Art Unit 1636  
 Remsen Building, Room 02A69  
 (571) 272-0772

RECEIVED  
 JUN 2 2004  
 (STIC)

Point of Contact:  
 Alexandra Waclawiw  
 Technical Info. Specialist  
~~GMT 6A02 Tel: 308-4491~~

Searcher: \_\_\_\_\_  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: 6-3-04  
 Date Completed: 6-3-04  
 Searcher Prep/Review: 7  
 Clerical: \_\_\_\_\_  
 Online time: 7

TYPE OF SEARCH:  
 NA Sequences: 8  
 AA Sequences: 1  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
 STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
 DRLink: \_\_\_\_\_  
 Lexis/Nexis: \_\_\_\_\_  
 Sequence Sys.: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (specify): computer

OM protein - protein search, using SW model  
 Run on: June 3, 2004, 07:04:28 ; Search time 23 Seconds  
 (without alignments)  
 Perfect score: 6294 seqs, 51625971 residues  
 Sequence: 1 MENTOKTIVPTGPPGYYA.....DEDFDLSGIPKHNITMEM 1203

Title: US-09-769-659-2 (without alignments)

2700.263 Million cell updates/sec

Scoring table: BLOSUM62 Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414 Minimum Match 0% Maximum Match 100%

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:\*

1: /cn2\_6/ptodata/2/iaa/5A/COMB.DEP:\*

2: /cn2\_6/ptodata/2/iaa/5B/COMB.DEP:\*

3: /cn2\_6/ptodata/2/iaa/6A/COMB.DEP:\*

4: /cn2\_6/ptodata/2/iaa/6B/COMB.DEP:\*

5: /cn2\_6/ptodata/2/iaa/PCITS.COMB.DEP:\*

6: /cn2\_6/ptodata/2/iaa/bactfiles1.DEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	3054	48.5	1452	4	US-09-127-227-2
2	183	2.9	35	2	US-09-332B-876-9
3	183	2.9	35	3	US-09-338-876-9
4	131	2.1	757	3	US-09-413-814-84
5	123	2.0	1074	1	US-09-071-035-354
6	123	2.0	1074	4	US-09-071-035-394
7	122	1.9	1096	4	US-09-134-000-5764
8	118	1.9	370	2	US-09-252-991A-16913
9	117	1.9	855	4	US-09-489-039A-12681
10	111	1.8	4630	4	US-09-091-609-2
11	111	1.8	5215	4	US-09-105-537-2
12	110	1.7	790	4	US-09-543-681A-6059
13	106	1.7	3567	2	US-07-642-734C-4
14	106	1.7	3567	3	US-08-439-009A-4
15	106	1.7	774	1	US-07-731-157A-7
16	106	1.7	774	2	US-08-541-180-7
17	105	1.7	1095	4	US-09-107-532A-3855
18	105	1.7	774	1	US-08-633-760-46
19	105	1.7	774	1	US-08-633-760-48
20	104	1.7	635	4	US-08-931-608A-5
21	104	1.7	635	4	US-09-851-847-5
22	104	1.7	774	1	US-08-019-870-5
23	104	1.7	1471	4	US-08-811-519-1
24	103	1.6	774	1	US-08-019-870-3
25	103	1.6	774	1	US-08-633-760-44
26	103	1.6	3472	4	US-09-408-020-4
27	102	1.6	729	1	US-08-070-165F-6

## ALIGNMENTS

RESULT 1  
 US-09-127-227-2  
 ; Sequence 2, Application US/09127227

; GENERAL INFORMATION:  
 ; Patent No. 6399334  
 ; APPLICANT: David M. Knipe  
 ; APPLICANT: Elizabeth McNamee  
 ; TITLE OF INVENTION: Replication-Competent Virus Expressing A  
 ; FILE REFERENCE: HU98-05  
 ; CURRENT APPLICATION NUMBER: US/09/127,227  
 ; CURRENT FILING DATE: 1998-07-31  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSSQ for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 1452  
 ; TYPE: PRT  
 ; ORGANISM: herpesvirus  
 US-09-127-227-2

Query Match 48.5%; Score 3054; DB 4; Length 1452;  
 Best Local Similarity 49.8%; Pred. No. 2.7e-304;  
 Matches 609; Conservative 200; Mismatches 366; Indels 48; Gaps 17;

Db 1 MENTQKTT--VPTGPIGLVY--ACRVEDDLEIISFLAARSTDSDLALLPLMRNITTE 55  
 Db 1 METKPTATTTIKVPGPGLVYVYARACPSRQI--LALLSARSDDADAVAPLVGVLT 58

Qy 56 KTFPTSSLAVVYSGARTGLAGAGITIKLTTSHYPYPSVYFHGGKHLVPLSSAAAPNULTRACNA 115  
 Qy 59 SGFEANAVVYVGSRITGGLGTTAVSLKLTHPSYHSSSSVYVHGGRHLDPSZQAPNULTRCER 118

Qy 116 ARERFGFSRCGQPPYDGAETTGABICTRIGLEPENTIILVLTALFKEARVMCNVFLHY 175  
 Db 119 ARRHRGFSDYTPRPGDLKHEETGEALCERIGDPRALIYLVTEGKFRAVCINNTFLHL 178

Qy 176 GGLDITHINNGDVIRIPLPVQLMFDPVNRVLPDPFNTTHRSIGGGFVYPTPPYNTGLCH 235  
 Db 179 GSSDKVTTGGAVSHRIPVYPLQLMFDPFNSVIAEPNAAHRSIGENFTPLPFENRPLNR 238

Db 236 LIHDCVIAPIAVALYRNTNTAVARGRAHHLAEDENHEGAVLFDITYTYFQSSSSGTTTAR 295  
 Db 239 LLFEAVYGAAPAVALCRNVDAAVARAAAHHLAEDENHEGAALPADITFTAAEASQG--KTR 296

Qy 296 GARRNDVNTSTSCKPSPGGFERLASSIMAAUTALHAEVINTGIXEETPDIKWPMPFGM 355  
 Db 297 GGR-----DGSGKGKGPAGFFQRLASMAGDALALESTISMAVEFDPPTDISAMPLCBEQ 351

Qy 356 EGTLPRLNAGLGYTAEVGIGAMVFSPLNSALYLVTEVEDSGMTAEAKDGGGPFSNRFYCF 415  
 Db 352 DTAARANANVGRAYLAAAGLIGAMFESTNSALHTEVDAGPDKHESK-PSYRFFLV 410

Qy 416 AGPHLARNPQTDRDGHVL-----SSQSTGSNTNTFSDYALICGFAPILLFL 468  
 Db 411 FGTHVAANPQDVREGHYVPGFGRPAPLPGGTQ-EFAGEHLMULCGFSPALLAKMFL 469

Qy 469 ERCDAGAFTGGCHG-DALKYTGTFDSEIPCSCLCEKHTPVGCAHTIVHRLQRMFRFGQT 527  
 Db 470 ERDGGTYIVGRDEMDFYRVAQDSDQPLGNYAPYLRLRKPGDQEAKMOTYRATLRLFIDLEQ 529

Qy 528 ROPIGVFGTMNSQYSDCPLGNYAPYLRLRKPGDQEAKMOTYRATLRLFIDLEQ 587

Db 530 RGAIGVFGTMNSQYSDCPLGNYAFAFSALKR-ADGSETARTIMQETYRATVMAELT 588

Qy 588 ERLLDRGAPCSSESSLGSSVIVDHPTRRILDTRAREQTTQEMKVLVETRDYKREGIS 647  
 Db 589 LQYDQAVPTANGRLETTITNREALHTVNNVQYDVEQLMNLVEGRNFKFRDGLG 648

RESULT 2  
 US-08-307-332B-9  
 ; Sequence 9, Application US/08807332B  
 ; GENERAL INFORMATION:  
 ; Patent No. 5959074  
 ; APPLICANT: Dreyfus, David H.  
 ; APPLICANT: Gelland, Erwin W.  
 ; TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF  
 ; TITLE OF INVENTION: GENE RECOMBINATION  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sheridan Ross  
 ; STREET: 1700 Lincoln St., Suite 3500  
 ; CITY: Denver  
 ; STATE: CO  
 ; COUNTRY: U.S.A.  
 ; ZIP: 80203  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/807,332B  
 ; FILING DATE: 28-FEB-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kovariik, Joseph E.  
 ; REGISTRATION NUMBER: 33,005  
 ; REFERENCE/DOCKET NUMBER: 2879-39  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/863-9700  
TELEFAX: 303/863-0223  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-807-332B-9

Query Match 2.9%; Score 183; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 545 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 579  
Db 1 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 35

RESULT 3 US-09-338-876-9  
Query Match 2.9%; Score 183; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11; Mismatches 0; Indels 0; Gaps 0;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 545 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 579  
Db 1 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 35

RESULT 3 US-09-338-876-9  
Query Match 2.9%; Score 183; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11; Mismatches 0; Indels 0; Gaps 0;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 545 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 579  
Db 1 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 35

RESULT 4 US-09-413-814-84  
Query Match 2.9%; Score 183; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11; Mismatches 0; Indels 0; Gaps 0;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 545 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 579  
Db 1 DPLGNAYAPYLILRKPGDQTEAAKATMDDTYRATLE 35

Query Match 2.1%; Score 131; DB 3; Length 57;  
Best Local Similarity 21.1%; Pred. No. 0.0012; Mismatches 251; Indels 212; Gaps 37;  
Matches 146; Conservative 84; Mismatches 251; Indels 212; Gaps 37;

Qy 545 VPKTFTSSLAVVSGART ---TGLAGGAGITKLTTSHFYPSPVVFHFGKHYLPSSAPNL 109  
Db 129 LERTLPVAVSIVADARAAALTSSAVAGIVAS-----LPASAA-- 167

Qy 110 TRACNAARERFGRFGRSPRCGPVPSAVETGAEICTRIGLEPENTILYVVTALFKEAIVFMC 169  
Db 168 ---ALQRQRLRWTATDQPS-RGPIEGFGA--- ALRPESV----- 198

Qy 170 NVFLHY ---GGLDIVHINHGDVIRIPLFPVQLFPMEDVNRLVPDPFTNHRHSIGEGFVY 224  
Db 199 -AFQYQTSSTGPKGWMLTHGNL---LENSRLIAHGFDLTSPDPY-----GVIW 244

Qy 225 PTPPYNTGLC-----HLIHDCVIAPMAYALR---VRNVTAV---ARGAAHLAFD-- 267

Db 245 LPPYHDMLLIGGILQALYRRIVALMSPSLQRPNWLRAVSALGASVSGGPNFAYDLC 304

Qy 268 ---ENHGAELVPPDITYTYFQSSSSSTTARGARDNVTNSTSKPEPGGTERLASSIMA 323  
Db 305 VRKSEEEERAAALD-----LSNWEVATGPVRAVSGVRE-AFYP 355

Qy 324 ADTALHAEVIENTGIGYEBTPDIKEWMFMEGTLPLRNALGSYTPARAVGIGAMVF-- 381  
Db 356 CYGLAELATLIVSGAREAPV-----LARLAEPEVLGRAVAAAE-GARFVG 403

Qy 382 ---SPNSALIYTTEVDGSMTEAKDGPSPSFRNRYQFASPHLA---ANPQTDRDGHV 432

Db 404 SGRALDPPA---VAIVDPA---NEIHPG-EIGEIM-VSSPSVAVGYGRPE----- 447

Qy 433 LSSQSTGSNTNTSVDLALIGGAGLILFLERCDAFAGCQHGDAKLYVITGT- 490  
Db 448 -----ETEATGATLAGSAAPR-----YLRTGDLGFLRQG-----LFTVGRSK 486

Qy 491 -----FSEIIPSLCBEH---TRPVC---AHITVHR.LQRM-----PREGOATRQ 529

Db 487 DLTLRGENHFPDIBETVSESSHRAVPGCSAASFVYHEGERLAVYCEVDPRV/ADPPE 546

Qy 530 PIGVGGTMSQYSQDPLGNYAPYLILRKPGDQTEAAKATMDDTYRATLE 35

REMARKS: The following table lists the results of the search. The results are listed in order of decreasing sequence similarity. The table includes the query sequence, the target sequence, the target sequence ID, the target sequence description, the target sequence length, the query sequence length, the score, the E-value, and the percentage identity. The table also includes the sequence alignment and the sequence identity matrix.

Query	Target	Target ID	Target Description	Target Length	Query Length	Score	E-value	Identity (%)	Sequence Alignment	Sequence Identity Matrix
547 IVAAEAVTIEHQ---LVAAVAAJIAAPGALPKISSGKTRRECRRAFE---DANGER	Db	Db	212 ---NIDYRVTGNQLVLT-----NSNSKGTLUKKSIGTGTG---VAYKK 251	598	598	547	1.0e-05	100	547 IVAAEAVTIEHQ---LVAAVAAJIAAPGALPKISSGKTRRECRRAFE---DANGER	Db
590 -----LLRGAPSESSGESSVIVDHPFERRILDTLARIEQTTQFMKVLUETRDYKI	Qy	Qy	466 FYLERDAGAFTGGHGDALKYVTGTFDSBIPCSLCEKHTRPVCAHTVHRLRQMRPFGQ 525	642	642	590 -----LLRGAPSESSGESSVIVDHPFERRILDTLARIEQTTQFMKVLUETRDYKI	Qy			
599 HVAFAPELLDQASPPD---APPETEPESSRLSALAR----TLARALRDAGQIDDA	Db	Db	252 AGLQTMAGALDKPNVYAIKINVEIKGS-LKIKDKESSDIVPTEVFLI-----DFGK 304	651	651	599 HVAFAPELLDQASPPD---APPETEPESSRLSALAR----TLARALRDAGQIDDA	Db			
643 ---REGI-SEATHSMALTPDPSGAFCPITNELL	Qy	Qy	526 A---TRQIGVFTOMNQYSDPDLNHY-----PVLURKGQDOTEAAKATM 570	671	671	643 ---REGI-SEATHSMALTPDPSGAFCPITNELL	Qy			
652 PISRFQDLSAALVELQHAFQYRTRGRAIPLTSIL	Db	Db	305 ALPSKQVTTDKGJ-----SILDQPHGTRVTEKSYVDPYDNTTPMAATIKAGETI 358	684	684	652 PISRFQDLSAALVELQHAFQYRTRGRAIPLTSIL	Db			
571 QDTYRATLERFLFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRRILDTLRA	Qy	Qy	571 QDTYRATLERFLFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRRILDTLRA 621	693	693	571 QDTYRATLERFLFIDLEQERLDRGAPCSSEGSL-----SVIVDHP-----FRRILDTLRA	Qy			
359 SMTSKRNMRQGQILIKTG-VEGTEGLDWNDSLAGNTFAIRKDSPAGIVQEITTDERG	Db	Db	359 SMTSKRNMRQGQILIKTG-VEGTEGLDWNDSLAGNTFAIRKDSPAGIVQEITTDERG 417	730	730	359 SMTSKRNMRQGQILIKTG-VEGTEGLDWNDSLAGNTFAIRKDSPAGIVQEITTDERG	Db			
629 RIEQTTOFMKVVLVETRDYKIREGLESATHSMALTPD-----YSGACPITNIFLYKRT	Qy	Qy	629 RIEQTTOFMKVVLVETRDYKIREGLESATHSMALTPD-----YSGACPITNIFLYKRT 675	761	761	629 RIEQTTOFMKVVLVETRDYKIREGLESATHSMALTPD-----YSGACPITNIFLYKRT	Qy			
418 RAE---TPKELANALELGTYVTE-TKSGNGFVNTPKTPKVELYQVALYTSVNSVNCQ	Db	Db	418 RAE---TPKELANALELGTYVTE-TKSGNGFVNTPKTPKVELYQVALYTSVNSVNCQ 473	809	809	418 RAE---TPKELANALELGTYVTE-TKSGNGFVNTPKTPKVELYQVALYTSVNSVNCQ	Db			
676 HLNADVDLAL-----SOCHVTFYQGQV-----EGMNRNQFQPVLRFRFDI	Qy	Qy	676 HLNADVDLAL-----SOCHVTFYQGQV-----EGMNRNQFQPVLRFRFDI 717	847	847	676 HLNADVDLAL-----SOCHVTFYQGQV-----EGMNRNQFQPVLRFRFDI	Qy			
474 NOETITGETTLLTKEKDGTGNESQGKAEFKGAEYTLFTAKDQAVRWSKEAK-----TEL	Db	Db	474 NOETITGETTLLTKEKDGTGNESQGKAEFKGAEYTLFTAKDQAVRWSKEAK-----TEL 526	925	925	474 NOETITGETTLLTKEKDGTGNESQGKAEFKGAEYTLFTAKDQAVRWSKEAK-----TEL	Db			
718 FNGGFPISTRSLTIVLSE-GPVYAPNPFLGQ-----DAPAGTRPDGLARVSV-----	Qy	Qy	718 FNGGFPISTRSLTIVLSE-GPVYAPNPFLGQ-----DAPAGTRPDGLARVSV----- 764	963	963	718 FNGGFPISTRSLTIVLSE-GPVYAPNPFLGQ-----DAPAGTRPDGLARVSV-----	Qy			
527 VKGTYKSDDEVTLAIDENKQAVKHLATNEYFWQETKKAEGYTLDETKYPSLKKYDNN	Db	Db	527 VKGTYKSDDEVTLAIDENKQAVKHLATNEYFWQETKKAEGYTLDETKYPSLKKYDNN 586	1001	1001	527 VKGTYKSDDEVTLAIDENKQAVKHLATNEYFWQETKKAEGYTLDETKYPSLKKYDNN	Db			
765 ---VIRLDIVRNRYV-----PSGNCTNLSIAA-----RARLYGLASAYQRQEKR	Qy	Qy	765 ---VIRLDIVRNRYV-----PSGNCTNLSIAA-----RARLYGLASAYQRQEKR 805	1039	1039	765 ---VIRLDIVRNRYV-----PSGNCTNLSIAA-----RARLYGLASAYQRQEKR	Qy			
587 KNAVITRDVTAKQVIRFGDFEFFKPGASDGTATGFDLSPKVSPLEXTETGAEDKA	Db	Db	587 KNAVITRDVTAKQVIRFGDFEFFKPGASDGTATGFDLSPKVSPLEXTETGAEDKA 646	1077	1077	587 KNAVITRDVTAKQVIRFGDFEFFKPGASDGTATGFDLSPKVSPLEXTETGAEDKA	Db			
806 VDMILHGAQF-----LLQKQFHGLLPRGM-----PPNSKS-----PNNP	Qy	Qy	806 VDMILHGAQF-----LLQKQFHGLLPRGM-----PPNSKS-----PNNP 838	1115	1115	806 VDMILHGAQF-----LLQKQFHGLLPRGM-----PPNSKS-----PNNP 838	Qy			
647 TTACNEQOLGPDGYQKFNLPYGDVLLIEEA---PFGFQKITHPLRIRSTFKENKDYAK	Db	Db	647 TTACNEQOLGPDGYQKFNLPYGDVLLIEEA---PFGFQKITHPLRIRSTFKENKDYAK 703	1153	1153	647 TTACNEQOLGPDGYQKFNLPYGDVLLIEEA---PFGFQKITHPLRIRSTFKENKDYAK	Db			
839 QWFWTLLQRNQ-----MPADLTHTEBTTIAAVKTEEEAANFINLNP-----PTCIGE	Qy	Qy	839 QWFWTLLQRNQ-----MPADLTHTEBTTIAAVKTEEEAANFINLNP-----PTCIGE 888	1181	1181	839 QWFWTLLQRNQ-----MPADLTHTEBTTIAAVKTEEEAANFINLNP-----PTCIGE	Qy			
704 BYVFITTEGOKQKPIKMTVPEYKLTNN-----FVSVLNRLMLYDLPEKEDSLTS	Db	Db	704 BYVFITTEGOKQKPIKMTVPEYKLTNN-----FVSVLNRLMLYDLPEKEDSLTS 754	1219	1219	704 BYVFITTEGOKQKPIKMTVPEYKLTNN-----FVSVLNRLMLYDLPEKEDSLTS	Db			
889 LAQFYMANLILKCYDHSOYLIINTLTSITGARRPRDPSVYLMTRKD---VTSAAIDIETQ	Qy	Qy	889 LAQFYMANLILKCYDHSOYLIINTLTSITGARRPRDPSVYLMTRKD---VTSAAIDIETQ 945	1257	1257	889 LAQFYMANLILKCYDHSOYLIINTLTSITGARRPRDPSVYLMTRKD---VTSAAIDIETQ	Qy			
755 LATWKGNKLNTLDETE-LVDKU-----RYNLHETKEDWVVAADIVDA-	Db	Db	755 LATWKGNKLNTLDETE-LVDKU-----RYNLHETKEDWVVAADIVDA- 799	1295	1295	755 LATWKGNKLNTLDETE-LVDKU-----RYNLHETKEDWVVAADIVDA-	Db			
946 AKALIETKENLPELWTAFST-----HLYRAAMNMRPMTYLGISTSKVHCA	Qy	Qy	946 AKALIETKENLPELWTAFST-----HLYRAAMNMRPMTYLGISTSKVHCA 992	1333	1333	946 AKALIETKENLPELWTAFST-----HLYRAAMNMRPMTYLGISTSKVHCA	Qy			
800 TKAQKDXEAKPVVIAETTATLANKERKGTVKWLHLRUTAEQ-----VLDKSVLTVNTV	Db	Db	800 TKAQKDXEAKPVVIAETTATLANKERKGTVKWLHLRUTAEQ-----VLDKSVLTVNTV 853	1371	1371	800 TKAQKDXEAKPVVIAETTATLANKERKGTVKWLHLRUTAEQ-----VLDKSVLTVNTV	Db			
993 AGNNRVPQAGNWSLQNGKRNQVCPLETFDRTRRPIACPRGGFICPVTGPSSGNRETTLSD	Qy	Qy	993 AGNNRVPQAGNWSLQNGKRNQVCPLETFDRTRRPIACPRGGFICPVTGPSSGNRETTLSD 1052	1409	1409	993 AGNNRVPQAGNWSLQNGKRNQVCPLETFDRTRRPIACPRGGFICPVTGPSSGNRETTLSD	Qy			
854 YENKVAEAGNE-----PVA-----KDASLNN	Db	Db	854 YENKVAEAGNE-----PVA-----KDASLNN 875	1447	1447	854 YENKVAEAGNE-----PVA-----KDASLNN	Db			
1053 QVRGIVTSGGAMVQLAIYATVRAVGR-----AQHMAFDWLSLTDEFLARDU-	Qy	Qy	1053 QVRGIVTSGGAMVQLAIYATVRAVGR-----AQHMAFDWLSLTDEFLARDU- 1102	1495	1495	1053 QVRGIVTSGGAMVQLAIYATVRAVGR-----AQHMAFDWLSLTDEFLARDU-	Qy			
876 QAQ-----TVNCNTTIEEVISQTKAHLEDSQFTFHDYMDNFDDVVTDVYDVLID	Db	Db	876 QAQ-----TVNCNTTIEEVISQTKAHLEDSQFTFHDYMDNFDDVVTDVYDVLID 923	1533	1533	876 QAQ-----TVNCNTTIEEVISQTKAHLEDSQFTFHDYMDNFDDVVTDVYDVLID	Db			
1103 -BELLHQIQTLETPTWTEGALEAKVILDE-----KTTAGD-----GETPMLAQNED	Qy	Qy	1103 -BELLHQIQTLETPTWTEGALEAKVILDE-----KTTAGD-----GETPMLAQNED 1149	1571	1571	1103 -BELLHQIQTLETPTWTEGALEAKVILDE-----KTTAGD-----GETPMLAQNED	Qy			
310 PSGGFERLALSIM-AADTAHLAIVTNTGIEEE-----TPTDIKEWDMFI	Qy	Qy	310 PSGGFERLALSIM-AADTAHLAIVTNTGIEEE-----TPTDIKEWDMFI 353	1609	1609	310 PSGGFERLALSIM-AADTAHLAIVTNTGIEEE-----TPTDIKEWDMFI	Qy			
105 PMSDIAKLVSLWEKAGTDITNNVAQMIWEVNGYKLHS1KRLGASVDTK-----	Db	Db	105 PMSDIAKLVSLWEKAGTDITNNVAQMIWEVNGYKLHS1KRLGASVDTK----- 158	1657	1657	105 PMSDIAKLVSLWEKAGTDITNNVAQMIWEVNGYKLHS1KRLGASVDTK-----	Db			
354 GMEGTLPLRNALGYSSTAR-----VAGVIG-ANVFSNPSALYTEVEDSGMTEAKDGG	Qy	Qy	354 GMEGTLPLRNALGYSSTAR-----VAGVIG-ANVFSNPSALYTEVEDSGMTEAKDGG 405	1705	1705	354 GMEGTLPLRNALGYSSTAR-----VAGVIG-ANVFSNPSALYTEVEDSGMTEAKDGG	Qy			
159 SIEGKINK-AIEEYQRKKSFRHNNTVKTILQGQSTTLDNEVNLSEPVXVONTA-----	Db	Db	159 SIEGKINK-AIEEYQRKKSFRHNNTVKTILQGQSTTLDNEVNLSEPVXVONTA----- 211	1753	1753	159 SIEGKINK-AIEEYQRKKSFRHNNTVKTILQGQSTTLDNEVNLSEPVXVONTA-----	Db			
406 GPSFNRFYQAGPFLAANPOTDRDGHVLSLSQSGSISNTFSDYLAICGEGAPILLR	Qy	Qy	406 GPSFNRFYQAGPFLAANPOTDRDGHVLSLSQSGSISNTFSDYLAICGEGAPILLR 465	1791	1791	406 GPSFNRFYQAGPFLAANPOTDRDGHVLSLSQSGSISNTFSDYLAICGEGAPILLR	Qy			

STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSDOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071, 035  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 REFERENCE/DOCKET NUMBER: PB369P2  
 ATTORNEY/AGENT INFORMATION:  
 NAME: A. Anders Brooks  
 REGISTRATION NUMBER: 36, 373  
 TELEPHONE: (301) 309-8504  
 TELEFAX: (301) 309-8512  
 INFORMATION FOR SEQ ID NO: 394;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1074 amino acids  
 TYPE: amino acid  
 STRANDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-071-035-394

Query Match 2.0%; Score 123; DB 4; Length 1074;  
 Best Local Similarity 18.3%; Pred. No. 0.016;  
 Matches 206; Conservative 150; Mismatches 415; Indels 352; Gaps 52;

Qy 250 RVRNNTAVGAAHLAFLDENHEGVLPPIITTYFQSSSSGTTGARRNDVNSTS KPS 309  
 Db 67 RTTSVUYAETGAKQTVFC-TEPGYSPITPEVTHGY-----QNP1 104

Qy 310 PSGGTRPLRNLGSYTA-----AAYDYLAVI FNTG YEE-----TPD1KEWMP1 353  
 Db 105 PSMDKAKLVSVLMEKAGTDIDTMVAQKCMIWEEVNGYKLHS1KRLGGASVDIK-----158

Qy 354 GMEGTLPLRNLGSYTA-----VAGYG-AMVSPNSN AYLTVEEDSGMTEAKDGGP 405  
 Db 159 SIEGINK-----AIEYQKKSFRNTVRLGQSPLD-----TPD1KEWMP1 353

Qy 406 GPSNPRFYQFAGPHLAANPQTDRGHVLSSQTSGSNTESFSDYLAJICGFGAPLLARLL 465  
 Db 212 -----NIDSRVIGNQLVLT-----NSNSRGTUTLKSAGTGTP-VAYKK 251

Qy 466 FYLERCDAAFTGKHDAKXVTFDSBIPCSLICEKTRPVCAHTTHRLBQMPFRGQ 525  
 Db 252 AGLCQVMAGLDKNTYA1KINVEKTKGS-LKIRKIDKEGSDIVPETYFHL-----DFGK 304

Qy 526 A-----TROP1GUVFGTMSQYSQDPLGNYA-----PYLLIRKPGDQTEAKATM 570  
 Db 305 ALPSKDVTIKDGI-----SILG1PHOTK1KITEKSVDPYMDTPMAM1KGETI 358

Qy 571 QDTYRATLERFLFIDLEQERLDRGAPCSSEGLS-----SVIDDHPT---FIRILDTLRA 621

Db 359 SMTSKM0RQGQILLEK7G-VETGDLWNDYSLAGNTFAIRKDSPACEIVQETIDEGK 417

Qy 622 RIECCTT0FMKVLYETRDYKIREGULSEATHSMALTFDP-----YSGAFCP1TNEFLYKRT 675

Db 418 RAE-----TPKEANALELGTYVTE-TKSNGFVNTPKTPKVELKIANQTVALTTSNTKQQ 473

Qy 676 HLAVYDQLL-----SOCHCVFYQGQV-----EGERNFRQFOPV1RRRFVDL 717

Db 474 NOETGETT1KEDDTGNEOSQKAEGFCAEYLTFTAKDQATKWSFKA-----TEL 526

Qy 718 FNGGF1STRSITVTLSE-GPVSAAPNPTLQG-----DAPAGRTEFDGDLARVSVE---- 764  
 Db 527 VRGTRASDETFLAIDKNCVAVKHLAINYFWQSTKAPAEYTLDETKPVS1KVDNNE 586

Qy 765 ---.VTRDIRVKRIVY-----PSGNCNTNLSE-----PAR1VGLASAYORQERK 805  
 Db 587 KNAVITRDVTAKEQVTRGFDFPKFAGSAGCTAETGFDLFSKVSPLEGTXEITGAEDKA 646

Qy 806 VDMLHGAJGF-----L1KQFHGLLFFRGM-----PPNSK-----PNP 838

Db 647 TTACNEQLGFDGKPKENLPGYKPEVYDYLJETRA-----PEGFOKITPLBIRSTFKENKDDYAKS 703

Qy 839 QWEFTLQORNO-----NPADKLTHEETTIAAVKRPFEEYAAINFNLP-----PTCIGE 888  
 Db 704 EYVFITTEEGKQPK1KMTVTPYKELTNE-----FVSYSLNRLMLYDLPEREDSLTS 754

Qy 889 LQOFYMANL1KUCDHSQYLINTLTSITGARRPRDPSSYLHTRKD-----VTSAADEITQ 945

Db 755 LATWKGZGKCKLNTLDFE-LVDKL-----RYNLHE1KEDWTYVAQ1DVEA- 799

Qy 946 AKALIEKTEENLPELWTAFT-----HLVRAAMNORPMVYLGISISKYHGA 992  
 Db 800 TKAQZERDExKARPVVIAETTANKEKOTSTWKL1LHKTAEQ-----VLDKSTVLFNYV 853

Qy 993 AGNNRYFQAGNWSGLNGKRNVCPLFTDPRTRPFIACPRGGFICPTVGPSSGNRETTLSD 1052  
 Db 854 YENKVAEAGNE-----PVA-----KDASLNN 875

Qy 1053 QVRGILVSGGAMVQLAIYATVRAVGA-----AQMFADWDLSLTDEF1ARDL-- 1102

Db 876 QAQ-----TVCNCTIERVSYIQTKAHEDGSCOTPHGDYMDMFDDVSYTHDVLQ 923

Qy 1103 -BEELDQIOTLEPPTWVGEALEAVK1LDE-----KTTAGD---GETPTNLAPNFD 1149

Db 924 GSKEAETILYALLPDDGTTKEIWKGK1KEEVNDKEFTKTVLAERKDTGKYPEGTKPTF- 982

Qy 983 -TEINYFEDGVNGNGKENEDLKEKSQSLTPKREVPTIPSTPKXOPE 1024

RESULT 7

US-09-134-000C-5764

Sequence 5764, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucerette-Stamm, et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812

SEQUENCE: Patent in version 3.1

SEQ ID NO: 5764

LENGTH: 1096

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-5764

Query Match 1.9%; Score 122; DB 4; Length 1096;

Best Local Similarity 18.5%; Pred. No. 0.02%; Mismatches 149; Indels 360; Gaps 53;

Matches 208; Conservative 149; Mismatches 410; Indels 360; Gaps 53;

Qy 250 RVRNNTAVGAAHLAFLDENHEGVLPPIITTYFQSSSSGTTGARRNDVNSTS KPS 309

Db 89 RTTSVUYAETGAKQTVFC-TEPGYSPITPEVTHGY-----QNP1 104

Qy 310 PSGGTRPLRNLGSYTA-----AAYDYLAVI FNTG YEE-----TPD1KEWMP1 353

Db 127 PMSMDKAKLVSVLMEKAGTDIDTMVAQKCMIWEEVNGYKLHS1KRLGGASVDIK-----180

Patent No. 651795  
 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196 136  
 CURRENT APPLICATION NUMBER: US/09/252, 991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074, 788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094, 190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 16913  
 LENGTH: 370  
 TYPE: PRT  
 ORGANISM: *Pseudomonas aeruginosa*  
 US-09-252-991A-16913

Query 354 GMEGTPLRNLAGGSYTA-----VAGVIG-AMVFSPSNALSALTYEVEDSGMTBEAKDGGP 405  
 Query 181 SIEGKINK-AIBEXQKRFSPNNTVTKTLLQGTSITLKDNEINLSEFDKVONTA----- 233  
 Database 406 GPSNRFYOFAGPHLAANPOTDUGHVLSSOSTGSNTTEPSVTDYLALJCGFGLAPLARLL 465  
 Database 234 ---NIDRVRGNLQLVLT-----NSNRSGTITLKSAGTGTp-VAYKK 273  
 Query 466 FYLERCDAGAFTGGHDAKYVGTGTFDSEBIPCSL-----CEKHTRPVCAHTTYVHLRQRMP 521  
 Database 274 AGLOTVMAGALDKPNTYAIK-----IDVETKGSKIKKIDKESSGDIVETVFL----- 322  
 Query 522 RFGAA-----TROPICVGTMNSQYSDDPDGLNYA-----PFLILRPGDQTEAA 566  
 Database 323 DFGRALPSKSDVTDKDG-----SILDQIPHGTKVLTTEKSVPDPMWDTPEMAATKA 376  
 Query 567 KATMDDTYATLRLFDILEQERLDRGAPCSSELS-----SVTVDHPT---FRTLD 617  
 Database 377 GETISMTSKMRQKGQILLEKGT-VETGTDLNDNYSLAGNTAIRDSPAGEIVQETT 435  
 Query 618 TLRARIEOTTOPMKVLYVETDRYKIREGLSEATHSMALTFDP-----YSGAFCPITNFL 671  
 Database 436 DEKRABE-TPKELIANAELGTVYTF-TKSSNGFNTFKPtkVELKyanQTVLVTSN 491  
 Query 672 VKRTHLAVQDL-----SQCHEVFYQQV-----EGRNFRNFGOPVLRRL 713  
 Database 492 VKGQNQETGETTKEKDGTGNESGKAEEYTLFTAKDQAYKWMSEALK----- 545  
 Query 714 FVDLFNGPPISTRSITVTLSE-GPVSAPNPNTLQ-----DAPAGRTFDGLARVSVE-- 764  
 Database 546 -TEVKGTGTADEVTTLADEKRNQVAVGHAINEYFNQETKAEGTYLDETKYPSIKV 604  
 Query 765 -----VIRDRVNRV-----PSGNCTNLSSEA-----PARLYGLASAYQR 801  
 Database 605 DNNEKNAVITRDYTAKEQVIRGFDFXPKAGSADGTAETGENDLSKVSPLESTNEITGA 664  
 Query 802 QERKVDMHFLGALG-----LLKQTHGLLPRGM-----PENSKS----- 835  
 Database 665 EDRATACNEQLGDFGKFKENLPGYDYLLEIA---PEGFKQITPLFIRSTPKENKDD 721  
 Query 836 -PNQOWFNTLQLRNQ-----MPADKLTHEBTITIAAVKRTEYTAINPFLP-PT 884  
 Database 722 YARSBYVFTITEBQKQP KMTVTPYELTNN-----PSVSLNRLMLDLPKEED 772  
 Query 885 CIGELAQFYMANLILKYCDHSQYLIINTLTSITGARRPRDPSSTVLMTRKD---VTSAAAD 941  
 Database 773 SLTSLATWDGNGKCLNTLDFTE-LVDKL-----RYNHEKEDVYVAQOID 818  
 Query 942 IETDKKALLEKTENLPELTTAFTS-----HIVRANMQRPMVYLGISISK 988  
 Database 819 VEA-TKAQEBKDEKAKPVVIAETTALANKETGTWKLHKLTAEQ-----VLDSKIVL 871  
 Query 989 YHGAQNNRVRQAGNWSGLNGKRNCPLETFDRTRPFLACPQGGFICPVTPGSSGNRET 1048  
 Database 872 FNTYVYENKTAPEANE-----PVA-----KDA 893  
 RESULT 9  
 Query 1049 TLDQYRGIVTSGGAMVQIAVYATVRAVGR-----ACINAFDWLSTDFDIFLAR 1100  
 Database 894 SLNQAO-----TVNCTIERHYSIQTCAHLEDGSQFTHGDMDFDVSYTH 941  
 Query 1101 DL---EEHDDOIICTLETPTWVGEALKVILDE-----KTAQD---GETPTNL 1145  
 Database 942 DVLDQSKAEPETIYLALLPDGTNKEWKSGKIEVNDKEFETKTVLAKVDIGKYPGK 1001  
 Query 1146 ENFEDCSEPSHDTTSNV-----UNISGNSISGTSVPGKLRPPEDE 1185  
 Database 1002 ETP---TEINKEODGVNGKHEDIKEKSQTLTPKVPPTPSTPKQPE 1046  
 Query 1003 ETP---TEINKEODGVNGKHEDIKEKSQTLTPKVPPTPSTPKQPE 1046  
 Database 1004 ETP---TEINKEODGVNGKHEDIKEKSQTLTPKVPPTPSTPKQPE 1046  
 RESULT 9  
 US-09-252-991A-16913  
 Sequence 16913, Application US/09/489039A  
 Patent No. 6610836  
 GENERAL INFORMATION:  
 APPLICANT: Gary Breton et. al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 FILE REFERENCE: 2709.2004001  
 CURRENT APPLICATION NUMBER: US/09/489, 039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: 1999-01-29  
 PRIOR FILING DATE: US 60/117, 747  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO 1681  
 LENGTH: 855  
 TYPE: PRT

; ORGANISM: Klebsiella pneumoniae  
 us-09-489-039A-12681

Query Match 1.9%; Score 117; DB 4; Length 855;  
 Best Local Similarity 21.8%; Pred. No. 0.042;  
 Matches 107; Conservative 54; Mismatches 140; Indels 190; Gaps 29;

Qy 320 SIMA----ADTAHAEVINTGTYBETPDIKEWPMFIGMEGTPLPRNALGTYTARYAG 374  
 Db 240 SIMARGDNTDTSLSLFGSLSN-GI -KLADEWRWQ-.GRGYAPEGVQASSARY- 292

Qy 375 VIGAMVFSPLSALVTEVEVSGMTAEKDGCPGP----SFNRFQ---- 414  
 Db 293 ---VIKQLGKVIVYETHVP----PGPFYIDLNTRVQDLOVQVIBANGKVS 337

Qy 415 -FAGPHLAANPOTDGD----HVLSSSTGSSNTF 446

Db 338 RFTVY-SAYDSVPGNMYAFAIGKVRQYRIDNRFLEGTLOHGVNNHHTLNGLSRA 396

Qy 447 VDYLALIGCGAPLLARLLFYLERDCAGA----TGG----HCD---- 482  
 Db 397 HDYQAWLA--GGVLLATRL----GAFGMNATWSGAQVEENDROQWRAFSYSKTF 445

Qy 483 ----PAVLYVGTF-SEIPEPSL-CRHTREVCAHTVHLRQMRPFCQATROPI 531  
 Db 446 STGTINVLVAAYRSTGGRDLEDFVGRQCEHNSITYVSTDHQ-RQLL--SATVSPL 501

Qy 532 GVGTMNSQYSDCDPLGNTAP----YLIRK 558

Db 502 GRIGLNLSAATDYNRKRITQLQLGNSNQWTKVSHCYNLAKQSTSDDGPFYHSTNE 561

Qy 559 PGDOTEAAKATMODYTATLRLF----IDLEQFLRDRGAPCSSEG---- 601  
 Db 562 PQDLMRQKCT-ETTSLSFTSIPPNWGDNTSVAMNNYNSR-ANRSTSLSMNGTRGEONE 619

Qy 602 LS-STVUDHDFR----JIDTLRARIETQTQFMKVIV--ETRDYK--IREGSLRAT 650  
 Db 620 LSWSVYGGYDVRYRNDEGTTATGGNVOQ-NTRFGALRYGYDQSKDVRQALGSSGSVVL 678

Qy 651 RSMALTFDPKS 661  
 Db 679 HSGGTTFGPRA 689

RESULT 10  
 US-09-091-609-2  
 ; Sequence No. 09091609  
 ; GENERAL INFORMATION:  
 ; PATENT NO. 6600029  
 ; CURRENT FILING DATE: 1998-06-19  
 ; EARLIER APPLICATION NUMBER: PCT/US96/20119  
 ; EARLIER FILING DATE: 1996-12-18  
 ; EARLIER APPLICATION NUMBER: 60/008,847  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO. 2  
 ; LENGTH: 4630  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces venezuelae  
 us-09-091-609-2

Query Match 1.8%; Score 111; DB 4; Length 4630;  
 Best Local Similarity 19.7%; Pred. No. 4.2;  
 Matches 250; Conservative 109; Mismatches 419; Indels 494; Gaps 66;

Qy 51 NLTVKETFTSSIAVV----SGARTTGLAGAGTILKLTTSFVPHGGKHKVLP 102  
 Db 166 SUTVDAQSSSLVAVLACESURAGESSTTAV-AGTNL-----NILA 206

Qy 103 SSAAPNLTTRACNAARERFGFSRCQGPVDDGAVETTGAEICUQLGLEPENTLYLVVTAFL 162  
 Db 207 ESA----VTEERPG----GLSPDGAYTFDARA-- 231

Qy 163 XEAVEMCNVFLHYCGLDIVHINHGDTYRIPFPVQFMPDVNLVYDPFNTTHRSIGEGF 222  
 Db 232 ----NGFREGG----GGVTVLKLPL-----SRALADGDRVH---GV 261

Qy 223 VYPTPFYNTGTLCHLINDCVIAFMVALVVRVNTAVARGAHLAFAFDENHEGAVLPPDITYT 282  
 Db 262 IRASAVNNDG----ATEGIVTPRRAAQKVLRAYKRALDPS-AVQ 303

Qy 263 YFQSSSGTTARGARRNDVNSTSKSPSPGGFERRLASIMAAATLHAEVFNTGTYEET 342  
 Db 304 XVELHGJGT----PVGDPLEAAALGAVLGSGARADEPL-----LVGSA 342

Qy 343 PTDIKEYPMFQGMEGTIPRNLALGSYTAVARVVGAVANVFSPNSSALVLYTEVEDSGMTEAKD 402  
 Db 343 KTNVGHLEGAGIVGLKTLALG--RRRIPASLNFRTPHDPL----DTLGLDVPD 394

Qy 403 GSGGSPSPNRFYQFAGPHIILANPQTDRD----GHVLLSQSTSNTNTBPSV 448  
 Db 395 G----LREVPHPDRELLAGVSSFGMGGTNAHVVLSEGAQGGGEGPGID 438

Qy 449 YALICFGGAPILLJFYLERDCAGA----FTGGBGDALK----YVTGTFDSEI-P 496  
 Db 449 EETPV----DSGALPPVVTGGEARAAQARLHEAVADEPLAP 480

Qy 497 CS1CEK--HTRPVCAHTTV----HRLRORMPRFGQATROPQIGFGTMNSQYSDCDPLG 548  
 Db 491 AALARSLLVTTTRVTHRSVLAIDPDRARLLDGLGALLAGTPAFGVVGT---- 528

Qy 549 NYAPYLILRKPGDQTEAKATMODYTATLRLFIDLEQFLRDRGAPCSSEGSSVTV 608  
 Db 529 ----PAPG----RLAVLF----SGQGQRTGNGM-ELIYAA 555

Qy 609 HPTFRLDTRDTRARIETTTQFMKVLPETRD----YKTRREGLSEATHSMALI 656  
 Db 556 HAPATAFDAAEELDLDLRLAELVAAGDTLDRTVHTOPALFAVEVALHLRVESWGV 615

Qy 657 FDYSGAFCPITNFLYERTHLLAVVQDIALSQCCHCVFYGOQVEGRNFRNOFOVLRFFVD 716  
 Db 616 PDLLAGH---SVGEISAAHVAGV--LSLRLA----ARLVAARGRLMQALP---- 656

Qy 717 LFNGGFISTRSTVTSSEGVSAPNPTLGODAAGTTGDLARYVEVIRVNRRVV 776  
 Db 657 --EGGAM---VAVEABEEVL--PHL----AGBRELSLAAVN-----GPPAVV 694

Qy 777 FSGNCNTNLSEAAARLVLGASAYQKRVDMHLHGAGFLKQFHGSLF---- 825  
 Db 695 LAG----AERAVLDVYELLREQGRKTRKLSVSHA-----FHPLMBPLDDFRVV 741

Qy 826 ----PR----GMPNPKSPNPKW----FWTLLQRNQMPADKLTHEBTITAAV 866  
 Db 742 EELDFQEPFRDVYVSTVGLPVA----GQWTDPEVW-----VQDQV-RPVRFLDAV 787

Qy 867 KRTEEEAAINFINLP----TCIGELAFCYMANLILKCDHQYLNLTSITGARRPRD 924  
 Db 788 -RTLEESGADTFLGDDGVCSAMAADS-----RQEAAATAVSALRKG--RP-E 833

Qy 925 PSSVLMNTRKDVTSAADIETOAKALEKTENLPELWTAFTSTHLYRAAMNORPMVTLGI 984  
 Db 844 POSLLAAUTTVFVRGHVVD----WTAHHSSTGTTRVPL----PTYAFQR 874

Qy 985 SISKYHAGAQNRRVQAGNWSLNGGKNCVCPVTCGGFICPVTGSSG 1044  
 Db 875 ERHWFDSAAARTAAPLTAGR-SCTGAG-----TGPAG 905

Qy 1045 -----NREITSDQVRGIIIVSGGAMVQIAIYATVRA-VGABA 1081



GENERAL INFORMATION:

APPLICANT: Katz, L. S. (Katz, L. S.)  
 APPLICANT: Donadio, S. (Donadio, S.)  
 APPLICANT: McAlpine, J. B. (McAlpine, J. B.)  
 TITLE OF INVENTION: Recombinant DNA Method for Producing Erythromycin Analogs  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSSEE: Edward H. Gorman  
 STREET: Abbott Laboratories D377/AP6D-2 One Abbott Park Rd  
 CITY: Abbott Park IL  
 STATE: IL  
 COUNTRY: US  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/642,734C  
 FILING DATE: 17-JAN-91  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dauckers, Andreas M.  
 REGISTRATION NUMBER: 32552  
 REFERENCE/DOCKET NUMBER: 4952.US.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-9396  
 TELEFAX: 708-938-2623  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3567 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-642-734C-4

Query Match 1.7%; Score 110; DB 4; Length 790;  
 Best Local Similarity 19.1%; Pred. No. 0.19;  
 Matches 171; Conservative 124; Mismatches 350; Indels 250; Gaps 42;

350 PMFIGMEGTL-  
 34 PLFVGREKSIHCLAAANDNKQIMLVAQKDASIDEPGVNDLFS-VGTVAVSLOMLKPDG 92

Qy 385 SALYLT-VEDSGMTEAKGGPGSFNRFYQAGPHILANPQTDRGHVLSSQSTGSNT 443  
 93 TKVVLVEGGRARRKLTLSQD----EFQKAXBYLDPFVYDREEQEVLRN----TAIN 142

444 EFSVDYLALICGAPILLARLFLYLERCDAGAFTGHH----GDALKY 486  
 143 QFE-GYIKLNKIKPEVLAASHALEESAKAATDTASHMPLKLKDQAVLEMDSYTERLEY 201

487 VTAGFDSEIFPCSLCEKHTPVCVAHTTVHRLQRMRP----FCAQATROPIGFGTANQ 540  
 202 LIMMNESEIDLQVEKIR----NRVKQNEKQSREYYLNEQMKAIQELGENDA 253

541 YSDCDPLGNAYAPYLJLRKPCDQTEAAKATMQD----TYRATLERFIDLEQBLRDR 593  
 254 PDENESSLKRKIE--AAKMPKREKTEAEIQLKNMSPMSAATVVRSTIDWVQ---- 306

594 GAPCSEGSSVIVDHPTRFLDTKLRARIEQTQFMKV----VETRDYKIREGISEAHTS 652  
 307 -VPNSR--SKVKKDVLVKQAEVLDHPTFLRQKPLKQVSRVSKIKGPI---- 357

653 MALTEDPYSS----AFCPDITNFLYRQHLLAVQDLSQCHCVYGOVEGENFRNQF 706  
 358 LCLVGPPGVKTSLSQGSIATKGRYVRAVGLGIRDEA----BIRGH---- 400

707 QPVLERRFDLFLNGERFISTSITVLESEGVSAPNPTLGDAPIRTRF----GDIARVSTB 764  
 401 ---RRTYISSLSSMPGKLIQNA----KVGKANPFLLEIDKMSDDMGRDPSALIS 448

765 VI----RDIRYKDR----YYFSGNCNTNLSSAA---RARLVLGLASAYQORQEKRVD 807  
 449 VLDPEONIATPDHYLVEDYDSDYRFAVTSNSMN PAPLDRMEYTRL-SGTYDEK-- 504

808 MHLHAGLGFLL KQFHGFLFRGMPNPKSPNQWPTLQRLQNPADKLTHETITIAAV 866  
 505 -LNIAKHQLJFKQ----TERRNALKENELTHDSAIMGII 538

867 KRFTEEYAAINF----NLPPTTIGELAQFYMANLILKCDQSOLINTLISITGARRPD 924  
 539 RYFTRE-AGFVSLERBISKLCKAYKOLLMDSTI---XHIBDENNLKDYL-GYRK--- 589

925 ESSVLIHWIRK----VTSAAIDETOAKALLEKTHENLPLWTAFT-STHLYRAAMNQ 976  
 590 ----VLYGRADTENRGMVTLGLATWEGGDLILITIASVPGKLTFTSISGEYMQESTQ 645

977 RPMVYLGISTSKYHGAGNNRVEQAGNWGLNGKNCVCPFLFTDFTRTRFLACPGGGFIC 1036  
 646 RAAITVYVRAARQL----GNG----DYEKRDHJHVPPEGA-T 679

1037 PVTGPSSGNRFT----LSDQVGRIVLVSQAGMOLIAATYVAVGAR---AQHMAF 1086  
 680 PKDGPBAGIAGCTALYSSLTGNCVPRSDVAMTG---BTLRQSVLPGIGLKEKLLAAHRRGG 736

1087 DDWLSLTDEFLFLDLEHDLQIQLTETPPTVGEALEAVLDEKTTAGGETP 1141  
 737 KTKVLFIDEN--KRDLEBIPENIVAD----IHPVTTIEVLTIALEKSP 781

Qy 1331 AGPVSVAVADV-DWFLVLSSEFAATP----TALFAELAGR 1365  
 Db 1283 -----ARGRSCTSYAWTTPWALPGAVDQGYLRLGRGLRS-ISADAMTRWVRLA 1330  
 Db 1336 GQQAEEPDs-GPTESEPAQRAGLSPDEQENNLLEVANVAE-----VLGHESSAEEINVR 1420  
 Qy 445 FSVDVLALICSGFAPLILFYLZERDAGAFTGSHGDAKYVTCFDSPECSLCERHT 504  
 Db 1421 RAFSEGGDSINAMARKR-----SASTG----LRPASL---- 1452  
 Qy 505 RPVCAHTVHLRQ--RMPREGQAOATRQPIGYFGTMNSQYSDCDP-----GNYA 551

RESULT 13  
 US-07-642-734C-4  
 Sequence 4 Application US/07642734C  
 Sequence 5 Application US/07642734C  
 Sequence 6 Application US/07642734C  
 Sequence 7 Application US/07642734C  
 Sequence 8 Application US/07642734C  
 Sequence 9 Application US/07642734C  
 Sequence 10 Application US/07642734C  
 Sequence 11 Application US/07642734C  
 Sequence 12 Application US/07642734C  
 Sequence 13 Application US/07642734C  
 Sequence 14 Application US/07642734C  
 Sequence 15 Application US/07642734C  
 Sequence 16 Application US/07642734C  
 Sequence 17 Application US/07642734C  
 Sequence 18 Application US/07642734C  
 Sequence 19 Application US/07642734C  
 Sequence 20 Application US/07642734C  
 Sequence 21 Application US/07642734C  
 Sequence 22 Application US/07642734C  
 Sequence 23 Application US/07642734C  
 Sequence 24 Application US/07642734C  
 Sequence 25 Application US/07642734C  
 Sequence 26 Application US/07642734C  
 Sequence 27 Application US/07642734C

Db 1453 -- VEDHPPTVTLAQHILRRLYGDQAAVRYGAAD-- --ESEPIAIVGIGCRPGGIGS 1506  
 Qy 552 PYLILR----- -KPGDQTEAA----- 566  
 Db 1507 PEGIWRVLAEGANLTGFPADRGWDIGRLYHDPDNGTSVYDVKCGFLDAADFDPGFFG 1566  
 Qy 567 ----- -KATHODTYRATLERFLIDLEQERLLDQAPCSSEBGLSIVIDHPTPR 614  
 Db 1567 ITPREALMDPOQLRMLETANTAAVEAGIDDALRSTDTSVFVGNGQSYBOMLLAGEER 1626  
 Qy 615 I----- -LDTLURARIEQT----- -TTQFMKVLYVETRDYKIRGSEATHSNAL 655  
 Db 1627 VDGXOGLNSASYLSGRLAYFEGWEGPAALTDACSSSLVGI - HLMQALRGECSLA 1684  
 Qy 656 T----- FDPIYSGAFCPTINFLVKRTHAVYQDIALSISQCHCVPQYGRNFRN----- 704  
 Db 1655 AGGYTNSDPT----- FVDFSTOR----- GLA-SDRCKASARAGFASEGVAA 1731  
 Qy 705 QFOPBLRFRFDLNGSFISTSRTSLSGPVSAAPNPLGODAPG---RFFGDILR 760  
 Db 1732 VLEPLSRA-----ANG-----HQVLAVLRSAAVNODGASNLGLAPNGPQERTVQALA 1782  
 Qy 761 VSVEVIRYKRVYVFSGNTCNLSAARARLVLGLASAYKORQEKR-----VDMILH----- 810  
 Db 1783 SGVPA-ADVDV--VEAHGTGTGELDPIEAS--ALIATYQDDRPLRUSVKINIGHTQ 1836  
 Qy 811 -----GALGFULKQPHGLLFRGKPNPSNPSNPNOMPAKDLTHEITIA 864  
 Db 1837 AALAAASVIVKUVALMEHML\_PRSHADELSPHIDW-----ESGAEVIREEVWPA 1887  
 Qy 865 AVKRFTEYRAAINFINIPTCIGELAQFYMANLILKYCHDSQYLIINTLTSITGARRPD 924  
 Db 1888 GSR---PRAGYSSFGVSGT-----NAHVIYEEAEO-----EAARTERG 1925  
 Qy 925 PSSVLMHMKDTSADIEQTOAKALLEKTENLPEI-----WTTAFTSTHLYRAAMNQR 977  
 Db 1926 PLPFLSRSRSEAAVAA---QARALAEHLDTPGLTDRAWLTLATGSRADFRAAV-- 1978  
 Qy 978 PMVGLGTSISKHGAQNNTYQAGNWGSLINGGNKVCPTDFTRRLIAIAPRGFCIP 1037  
 Db 1979 -----LGDDRGAVCAELDAEGR-----PSADAVAP 2005  
 Qy 1038 VTGPSSGRRETTLSDVGRGLIVSGGAMQDIAVYVRAVGAQAHMAYDDNWSLTDEE 1097  
 Db 2006 VT---SAPRKVU-----VFPQGQA-----WVG----- 2026  
 Qy 1098 LARDLBLEHDLQIOTL-----ETPNTVGEALEAVKILDEKTTAGD 1138  
 Db 2027 MARDLSESEVFAEMSRSRCAEALSPTHDN-----KLID--VVREGDG 2065  
 Db 2081 RAEFSLGDSLNAMALRBL-----SASIG-----LRIPLASL----- 1452  
 Qy 505 RPVCAHTTWRLRO--RMRFRGTAOTRDPGIGTMSQYSDCDPL----- -GNYA 551  
 Db 1453 --VEDHPPTVTLAQHILRRLYGDQAAVRYGAAD-- --ESEPIAIVGIGCRPGGIGS 1506  
 Qy 552 PYLILR----- 566  
 Db 1507 PEQIWRVLAEGANLTGFPADRGWDIGRLYHDPDNGTSVYDVKCGFLDAADFDPGFFG 1566  
 Qy 567 ----- -KATHODTYRATLERFLIDLEQERLLDQAPCSSEBGLSIVIDHPTPR 614  
 Db 1567 ITPREALMDPOQLRMLETANTAAVEAGIDDALRSTDTSVFVGNGQSYBOMLLAGEER 1626  
 Qy 615 I----- -LDTLURARIEQT----- -TTQFMKVLYVETRDYKIRGSEATHSNAL 655  
 Db 1627 VDGXOGLNSASYLSGRLAYFEGWEGPAALTDACSSSLVGI - HLMQALRGECSLA 1684  
 Qy 656 T----- FDPIYSGAFCPTINFLVKRTHAVYQDIALSISQCHCVPQYGRNFRN----- 704  
 Db 1655 AGGYTNSDPT----- FVDFSTOR----- -GLA-SDRCKASARAGFASEGVAA 1731  
 Qy 705 QFOPBLRFRFDLNGSFISTSRTSLSGPVSAAPNPLGODAPG---RFFGDILR 760

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/439,009A  
 FILING DATE: 11-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Casuto, Dianne  
 ADDRESS: 40, 943  
 REFERENCE/DOCKET NUMBER: 4952-US.D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847-938-3137  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3567 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-439-009A-4

Query Match 1.7%; Score 106.5; DB 3; Length 3567;  
 Best Local Similarity 19.9%; Pred. No. 7.4;  
 Matches 237; Conservative 104; Mismatches 384; Indels 465; Gaps 62;  
 Matches 237; Conservative 104; Mismatches 384; Indels 465; Gaps 62;

Qy 125 CGQPPVDAVETTGE---ICTR-----LGDEPENTILYLVVTALFKEAVFMCNVFLH 174  
 Db 1165 CGDDLLAEEAGASAVVCAQDAAALEALGDEP-----VTAI-----VH 1205  
 Qy 175 YGGDIDVHINHGDYTRIPLFPVQLFMPDVNRALYDPDPFTNTHRSIGEGFVYPPFPYNTGLC 234  
 Db 1206 AGTL---TNFG-----SISVEAPEEF-----AETIAAKTALL 1234

Qy 235 HLHIDCVIAFMAYALRV-----RNTAVARSAEABL\_AFDENHEGAVLPPDITYT 282  
 Db 1235 AVL--BVLDGRAYREVYSSVAGIWWGAGMAYAASAYVLLAETHR----- 1282

Qy 283 YFQSSSSGTTARGARRNDVNSTSKPSPSG-----GF--ERRLASTMAADTALHA-EVIFN 335  
 Db 1283 -----ARCSCTSVAITPAWALIQQGAVDGRGERS-LADARMTWERYLA 1330

Qy 336 TGTYBETPTDIKBNPMFI\_GMCETLPRINALGSYTAVAGVIGMVSNSAIVLYTEVED 394  
 Db 1331 AGPVSVAADV-DMPVLSRGFAATRP----- 1365

Qy 395 SGHTEAKOOGPSFRNFTQFAG-----PHILANPQDRTGIVLSSOSTGSNTNE 444  
 Db 1366 GGQAEAEPS-GPTGEPAQRLAGLSPDEQENILEVANAYE-----VLGHESSAASINVR 1420

Qy 445 FSVDVLALICFGGAPLLRLFTYLERDAGFTGHDALKVVTGTDSE-EPCLCERHT 504  
 Db 1421 RAFESLGLDSLNAMALRBL-----SASIG-----LRIPLASL----- 1452

Qy 505 RPVCAHTTWRLRO--RMRFRGTAOTRDPGIGTMSQYSDCDPL----- -GNYA 551  
 Db 1453 --VEDHPPTVTLAQHILRRLYGDQAAVRYGAAD-- --ESEPIAIVGIGCRPGGIGS 1506  
 Qy 552 PYLILR----- 566  
 Db 1507 PEQIWRVLAEGANLTGFPADRGWDIGRLYHDPDNGTSVYDVKCGFLDAADFDPGFFG 1566  
 Qy 567 ----- -KATHODTYRATLERFLIDLEQERLLDQAPCSSEBGLSIVIDHPTPR 614  
 Db 1567 ITPREALMDPOQLRMLETANTAAVEAGIDDALRSTDTSVFVGNGQSYBOMLLAGEER 1626  
 Qy 615 I----- -LDTLURARIEQT----- -TTQFMKVLYVETRDYKIRGSEATHSNAL 655  
 Db 1627 VDGXOGLNSASYLSGRLAYFEGWEGPAALTDACSSSLVGI - HLMQALRGECSLA 1684  
 Qy 656 T----- FDPIYSGAFCPTINFLVKRTHAVYQDIALSISQCHCVPQYGRNFRN----- 704  
 Db 1655 AGGYTNSDPT----- FVDFSTOR----- -GLA-SDRCKASARAGFASEGVAA 1731  
 Qy 705 QFOPBLRFRFDLNGSFISTSRTSLSGPVSAAPNPLGODAPG---RFFGDILR 760

RESULT 15  
 US-07-731-157A-7  
 Sequence 7, Application US/07731157A  
 Parent No. 557032  
 GENERAL INFORMATION:  
 APPLICANT: Quax, Wilhelmus J.  
 APPLICANT: Missel, Onno  
 APPLICANT: Van der Laan, Jan M.  
 APPLICANT: Lenting, Herman B. M.  
 TITLE OF INVENTION: Mutated beta-lactam acylase genes  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM  
 STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94016  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.26 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/731,157A  
 FILING DATE: 19910509  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 90200962  
 FILING DATE: 18-APR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: RAE-VENTER PH.D., BARBARA  
 REGISTRATION NUMBER: 32,750  
 REFERENCE/DOCKET NUMBER: GBRO-027/000US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-494-7622  
 TELEFAX: 415-857-0663  
 TELEX: 380816 COOLBY PA  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids

TYPE: AMINO ACID  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 Pseudomonas species  
 STRAIN: SE83  
 US-07-731-157A-7  
 Query Match 1.7%; Score 106; DB 1; Length 774;  
 Best Local Similarity 20.2%; Pred. No. 0.47; Mismatches 251; Indels 242; Gaps 37;  
 Matches 145; Conservative 79; Query 258 ARGAALAFDENHEGAV-LPDIDITYFQCSSSGTTARGARRDYNSTEKPSPEGFER 316  
 Db 183 ANALKRYDGGDQDUCIPPGVEALERADLAIRPAVIDALLKAMGDDSAAGGSNN 242  
 Qy 317 ---RILS---IMADDTALHAEVIFNTGTYBETPTDIKEWPMGCTILPRUNALGS 367  
 Db 243 WAWAPRGTATERPILLADPHRVEI---PENYAQHLACDRFDM-TG---TVP----- 289  
 Qy 368 YTARVAVIGAVANFSPNSA-----LYTLEVEDSGMTE----- 399  
 Db 290 -----GVPGFPHFAINGKRYAVYCUTHAFMIDHDLYLEQFAEDGTRARFGNEFEPVAWRRD 343  
 Qy 400 --AKDGGPSPSNTRFYQAGPHALAAQPTQDGDHVLSQSSTGSNTFESTYDYLALICGFF 457  
 Db 364 RIAVRGGADREDIVETRHPVIAGD-----LEGALITLRSYQFAEDLSFCLTRMP--G 398  
 Qy 458 APILLARLFYLERCDAAGFTG-GH---GDALKYTTGTFDSEIPOSLCERHTRPVCAHT 511  
 Db 399 ASTVAQY-----DATRGWGLIDRNIVAGDVAIGVAGS1GHLRARVSPRENGWLPGWMS 452  
 Qy 512 TYHLR-----QMRMPGQATROPICFGTGMNSQY-----SDCDPLGNAYAP--- 553  
 Db 453 GEHEWGRWIPHAMPYR---VTDPPGGLIVTANRVAADDHPDYLCTDCHP----PYRAE 504  
 Qy 554 ---LILRKPGDQTEAKATHDT-----YRATLERLFI-DIICERL----- 590  
 Db 505 RIMERLIVASPAVDDAAIAHDTLSSPHVGLLARLALGICQSLPPEELRQTLIADWGR 564  
 Qy 591 LDORGAPCSSEGGSVIVDHPFRILDTLARIEQTITQFMKVLYVTDYKIREGLSEA- 649  
 Db 565 MDAGSQARSA-----YNAFRL-----TRLYTARSQHQA1 596  
 Qy 650 THSMALT---FDPYSGAFCPITFLNVRTHLAVVQ---DIALSQCICVFGQVQEGRNF 702  
 Db 597 AHPPAAVPPGVSPOQQTWAVPT-LIANDDAGMLKGMSWDEALSEALSV-ATQNLTRGRW 654  
 Qy 703 RNOQPVIRRFRYDLENGGETISTRITVTLSEGSPVSP-----NPTLGODAP 749  
 Db 655 GEEIRP---RFTHPLAQOFPAWALL----NPVSSPIGGGDTVLANGLVPSAGEBAT 705  
 Qy 750 AGRTFDGDLARVSVEVTDIRVKNRYVFS-GNCTNLSEARARLVGLASAYQRQEKVDM 808  
 Db 706 YG-----ALSRYFDVGNWDN-----SRWVV 726  
 Qy 809 LHGLALGFLLKQFHGFLLPRGMPPNSKSNSPNQW-----FWTLLQRNQMPADKLTHEE1 860  
 Db 727 FHGASG-----HPASPHYADQNAAPNSDCANVPMLYSWDRRAAEAVTSQEL 771

RESULT 16

US-08-541-780-7  
 Sequence 7, Application US/08541780  
 Patent No. 5935331  
 GENERAL INFORMATION:  
 APPLICANT: Quax, Wilhelmus J.  
 APPLICANT: Missel, Onno  
 APPLICANT: Van der Laan, Jan M.  
 APPLICANT: Lenting, Herman B. M.  
 TITLE OF INVENTION: Mutated beta-lactam acylase genes  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM  
 STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94016  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.26 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/731,157A  
 FILING DATE: 19910509  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 90200962  
 FILING DATE: 18-APR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: RAE-VENTER PH.D., BARBARA  
 REGISTRATION NUMBER: 32,750  
 REFERENCE/DOCKET NUMBER: GBRO-027/000US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-494-7622  
 TELEFAX: 415-857-0663  
 TELEX: 380816 COOLBY PA  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids

1 CORRESPONDENCE ADDRESS:  
 1 ADDRESS: COOLEY GODWARD CASTRO HUDDLESON & TATUM  
 1 STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR  
 1 CITY: PALO ALTO  
 1 STATE: CALIFORNIA  
 1 COUNTRY: USA  
 1 ZIP: 94306

1 COMPUTER READABLE FORM:  
 1 MEDIUM TYPE: Floppy disk  
 1 COMPUTER: IBM PC compatible  
 1 OPERATING SYSTEM: PC-DOS/MS-DOS  
 1 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

1 CURRENT APPLICATION DATA:  
 1 APPLICATION NUMBER: US/08/541,780  
 1 FILING DATE:  
 1 CLASSIFICATION: 435  
 1 PRIOR APPLICATION DATA:  
 1 APPLICATION NUMBER: US/07/731,157  
 1 FILING DATE:  
 1 ATTORNEY/AGENT INFORMATION:  
 1 NAME: RAE VENTER PH.D., BARBARA  
 1 REGISTRATION NUMBER: 32,750

1 REFERENCE/DOCKET NUMBER: GBRO-027/00 US  
 1 TELECOMMUNICATION INFORMATION:  
 1 TELEPHONE: 415-494-1622  
 1 TELEFAX: 415-857-0663  
 1 TELEX: 380816 COOLEY PA

1 INFORMATION FOR SEQ ID NO: 7:  
 1 SEQUENCE CHARACTERISTICS:  
 1 LENGTH: 774 amino acids  
 1 TYPE: amino acid  
 1 TOPOLOGY: linear  
 1 MOLECULE TYPE: protein  
 1 HYPOTHETICAL: NO  
 1 ORGANISM: Pseudomonas species  
 1 STRAIN: SE83

1 US-08-541-780-7

1 Query Match 1.7% Score 106; DB 2; Length 774;  
 1 Best Local Similarity 20.2%; Pred. No. 0, 47; Mismatches 21; Indels 2,2; Gaps 37;  
 1 Matches 145; Conservative 79; Insertions 21; Deletions 21; Length 774;

Qy 258 ARGAAHLADEFNEEGAV-LPPDITYYPOSSSGTTARGARRNDVNSTKSPSPGGFER 316  
 Db 181 AAANALKURYDDGGDLCLCPGTYEARLADALALRPAVDALLKANGDASDAAGGSNN 242

Qy 317 -----RLS---IMAADTAHLAEVINTGIVYBTPDIKEKPMFICMGTIPRNLALGS 367  
 Db 243 WAWAPGRTITGRPLAGDHRVEI---PGMYAQHHLACDRDM-1GL-TVP----- 289

Qy 368 YTARVAGYVIGAMYFSPNSA-----LYLTTEVEDSGMTE----- 399  
 Db 290 -----GVEGPFPFAHNGKVAICYTHAMDIDLYLQFAEDORTARFNGEEFPVWRD 343

Qy 400 --AKDGGPPSPNRFYQFAGPHLAANPOTDRDGHVLSQSTGSSNTFSTVDYLALICGFG 457  
 Db 344 RIAVRGGADREFDIVETRGPVAGDP--LEGAALTLSRSQFAETDLSFDLTRNP--G 398

Qy 458 APILLARLFLYLERCDAGATG-GH-----GDALKYVGTGDFSEIPCSUICEKTRPICAHT 511  
 Db 399 ASTVPAQLY-----DATRKGGLDHNLYAGDVAISGHLVRAVSPRENSWLPVGWS 452

Qy 512 TVHLR---QRMPRFGQATROPIGVFGTMNSQY-----SDCDPLGNYAPY-- 553  
 Db 453 GEHWQRGNWPHAMPR---VIDPFGGLVITANNRVRVADHPDYLCTCHP----PYRAE 504

Qy 554 ---LILRKPGDQPEAAKTMQDT----KATLRLPFI---DLEOPRL----- 590

Db 505 RIMERLVAASPAAVDDAAAHADTLSPHYGLLARLRLAIGQSSLPAELRQTLIAWDR 564

1 Query Match 1.7% Score 105.5; DB 4; Length 1095;  
 1  
 1 591 LDGAPCSSEGSSVIVDHPTRRILDTLARIEQTTOQMVKVLERDYKIREGLSEA- 649  
 1 565 MDASQAAA-----YNAFRAA-----TRLVTAWSGLEQAI 596  
 1 650 THSMALT---FDPYSGAFCPITNLFVKRTHLAVQ---DLAISQCHVFYGOVEGEMNF 702  
 1 597 AHPPAVPQGVSPGQVWAVPTLLRNDDAGMLKGNSWDEALSEALSV-ATCNLTGRW 654  
 1 703 RNOQFPIVLERRFYDLENGFISRTSIVTTLSEGVPSSAP-----NPFLGQDAP 749  
 1 655 GBEHP---RFTHPLSAQPPAAALL---NPVSPRPIGGDGTVLANGLYPSAGFBAT 705  
 1 750 AGRTFDDGDLARVSYTENVDIRVGNRVS-GNCTNLSSPAAARLVLGLASAYOQERKRYDM 808  
 1 706 YG-----ALSRVYDVGNDN-----SRWV 726  
 1 809 LHGALFLIKQPHGLFPRGMPNPKSNPQW---FWTLLQRNOMPAEKLTHEEI 860  
 1 727 FHGASG-----HPASPHYADONAPNSDCAAVPMLYSWDRTAEEAVTSQEL 771

1 RESULT 17  
 1 US-09-107-532A-3855  
 1 ; Sequence 3855, Application US/09107532A  
 1 ; Patent No. 6583275  
 1 ; GENERAL INFORMATION:  
 1 ; APPLICANT, Lynn A Doucette-Stamm and David Bush  
 1 ; TITLE OF INVENTION: AMINO ACID SEQUENCES RELATING TO  
 1 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 1 ; NUMBER OF SEQUENCES: 7310  
 1 ; CORRESPONDENCE ADDRESS:  
 1 ; ADDRESS: GENOME THERAPEUTICS CORPORATION  
 1 ; STREET: 100 Beaver Street  
 1 ; CITY: Waltham  
 1 ; STATE: Massachusetts  
 1 ; COUNTRY: USA  
 1 ; ZIP: 02454  
 1 ; COMPUTER READABLE FORM:  
 1 ; MEDIUM TYPE: CD/ROM ISO9660  
 1 ; COMPUTER: PC  
 1 ; OPERATING SYSTEM: <Unknown>  
 1 ; SOFTWARE: ASCII  
 1 ; CURRENT APPLICATION DATA:  
 1 ; APPLICATION NUMBER: US/09/107,532A  
 1 ; FILING DATE: 30-Jun-1998  
 1 ; PRIORITY APPLICATION DATA:  
 1 ; APPLICATION NUMBER: 60/085,598  
 1 ; FILING DATE: 14 May 1998  
 1 ; APPLICATION NUMBER: 60/051571  
 1 ; FILING DATE: July 2, 1997  
 1 ; ATTORNEY/AGENT INFORMATION:  
 1 ; NAME: Arinello, Pamela Denice  
 1 ; REGISTRATION NUMBER: 40,489  
 1 ; REFERENCE/DOCKET NUMBER: GTC-012  
 1 ; TELECOMMUNICATION INFORMATION:  
 1 ; TELEPHONE: (781) 893-5007  
 1 ; TELEFAX: (781) 893-8277  
 1 ; INFORMATION FOR SEQ ID NO: 3855:  
 1 ; SEQUENCE CHARACTERISTICS:  
 1 ; LENGTH: 1095 amino acids  
 1 ; TYPE: amino acid  
 1 ; TOPOLOGY: linear  
 1 ; MOLECULE TYPE: protein  
 1 ; HYPOTHETICAL: YES  
 1 ; ORIGINAL SOURCE:  
 1 ; ORGANISM: Enterococcus faecium  
 1 ; FEATURE:  
 1 ; NAME/KEY: misc feature  
 1 ; LOCATION: (B) LOCATION 1..1095  
 1 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3855:  
 1 ; US-09-107-532A-3855

Best Local Similarity 18.9% ; Prod. No. 1 ; Matches 145 ; Conservative 112 ; Mismatches 298 ; Indels 211 ; Gaps 35 ;		Best Local Similarity 18.9% ; Prod. No. 1 ; Matches 145 ; Conservative 112 ; Mismatches 298 ; Indels 211 ; Gaps 35 ;	
y	551 APLILRKHGQDEAAKATMDQTYRATERLRLPDLDEQERPLLRDQGAPCSSEGUS-----S 604	y	551 APLILRKHGQDEAAKATMDQTYRATERLRLPDLDEQERPLLRDQGAPCSSEGUS-----S 604
o	360 APTIDTPMTTIIKAGETIVYTTSKNAEKGQIIIDKSSG-VETGSDLWNDNYSLAGNTFA 418	o	360 APTIDTPMTTIIKAGETIVYTTSKNAEKGQIIIDKSSG-VETGSDLWNDNYSLAGNTFA 418
y	605 VIVDHPPTFRILDL-TLRARIEQTTQFMKVLYVETRDYKIREGISEAATHSMALTEDP---- 659	y	605 VIVDHPPTFRILDL-TLRARIEQTTQFMKVLYVETRDYKIREGISEAATHSMALTEDP---- 659
o	419 IRKDSPTGIVQENTTDENGHAETPKANALEGLTYVTE--TKASHGFNTFKPVKE 476	o	419 IRKDSPTGIVQENTTDENGHAETPKANALEGLTYVTE--TKASHGFNTFKPVKE 476
y	660 -YSGAFCPITNPLVKRTHAVYQDLA-----SQCCHVYFGQV----EGR- 700	y	660 -YSGAFCPITNPLVKRTHAVYQDLA-----SQCCHVYFGQV----EGR- 700
o	477 LK1ANQTVLAVTWSVKGQNEQVETGETTITKEDKDGDKAQGRAVFEIGEYTLPTADKGKA 536	o	477 LK1ANQTVLAVTWSVKGQNEQVETGETTITKEDKDGDKAQGRAVFEIGEYTLPTADKGKA 536
y	701 -NFRNQFQPVYLRRFVLDLNGGFTSSTRSITVILSEGPYSAP----NPTLQGD-APAGR 752	y	701 -NFRNQFQPVYLRRFVLDLNGGFTSSTRSITVILSEGPYSAP----NPTLQGD-APAGR 752
o	537 VKNSEFKP-----EYVKGTVKASDETVLALDEKNGA2A9VHLAIEYVWYBTKAEGY 589	o	537 VKNSEFKP-----EYVKGTVKASDETVLALDEKNGA2A9VHLAIEYVWYBTKAEGY 589
y	753 TFDSDLARYSVE-----VTRDIRVYKTRVV-----FSGNCTNLSEIA----- 788	y	753 TFDSDLARYSVE-----VTRDIRVYKTRVV-----FSGNCTNLSEIA----- 788
o	590 TLDETKYPISIIKVVDDNEKNAVITRDYTAKEQIIRGFDFFRPAGGAAAGTATGFDNLTF 649	o	590 TLDETKYPISIIKVVDDNEKNAVITRDYTAKEQIIRGFDFFRPAGGAAAGTATGFDNLTF 649
y	789 -RARIYGLASAYOREKRYDMLHGAJGF-----LLKQFEGLILPFRGM---- 829	y	789 -RARIYGLASAYOREKRYDMLHGAJGF-----LLKQFEGLILPFRGM---- 829
o	650 KVSPPLGEGNEITGABEATTAINEQQLGFDGYKGFENLYQGDYLLEVEA--PEGFGKIKT 706	o	650 KVSPPLGEGNEITGABEATTAINEQQLGFDGYKGFENLYQGDYLLEVEA--PEGFGKIKT 706
y	830 PPNSKSP-----NPQWFVLLLQRNQ-----MPADKLTHEETTIAAVKRKTEE 872	y	830 PPNSKSP-----NPQWFVLLLQRNQ-----MPADKLTHEETTIAAVKRKTEE 872
o	707 PLEIRSTFKENKEDEPVKSPIVFTIETQDKQPIKTVTYPKEKLN-----KAISVS 757	o	707 PLEIRSTFKENKEDEPVKSPIVFTIETQDKQPIKTVTYPKEKLN-----KAISVS 757
y	873 YRAINFINLP-PTCIGELAQFMANLILKYCDHSQYLNINTLTSITGARRPRDPSSTVLH 930	y	873 YRAINFINLP-PTCIGELAQFMANLILKYCDHSQYLNINTLTSITGARRPRDPSSTVLH 930
o	758 LNRLMLYDLPFEEEDSLTSLSLATWDKGNEKLTSLSTE-LVDKL-----SYNLH 803	o	758 LNRLMLYDLPFEEEDSLTSLSLATWDKGNEKLTSLSTE-LVDKL-----SYNLH 803
y	931 WIRKD---VTSAAIDIETQAKALLEKTENDPELATTAFSTHLYRAANN----QRPVW-- 980	y	931 WIRKD---VTSAAIDIETQAKALLEKTENDPELATTAFSTHLYRAANN----QRPVW-- 980
o	804 EIKEDWVYVAQAIQDA-TKAQAEKDEKAKPV-VIAETSATLANKEKEKGWTQIHKITAE 861	o	804 EIKEDWVYVAQAIQDA-TKAQAEKDEKAKPV-VIAETSATLANKEKEKGWTQIHKITAE 861
y	981 -VUGISIISKYHGAGNNRYFOAGNWSGLNGKNCVPLFTEDRTRFIIACPRGGFFICPVT 1039	y	981 -VUGISIISKYHGAGNNRYFOAGNWSGLNGKNCVPLFTEDRTRFIIACPRGGFFICPVT 1039
o	862 QVLNKNTIVLNFYVNEKNAEFGD-----KPVVA-----KPVVA 889	o	862 QVLNKNTIVLNFYVNEKNAEFGD-----KPVVA-----KPVVA 889
y	1040 GPSSGNRETTLSDQVRGILIVSGGAMVLAIVATVRAVAGARAQHMAFDWLSLTDDFLA 1099	y	1040 GPSSGNRETTLSDQVRGILIVSGGAMVLAIVATVRAVAGARAQHMAFDWLSLTDDFLA 1099
o	890 -----KDVSLLNQQTVCQTVCVHEVSTQTKAHLENG----SOTFTHGDDVMDFDVSIT 939	o	890 -----KDVSLLNQQTVCQTVCVHEVSTQTKAHLENG----SOTFTHGDDVMDFDVSIT 939
y	1100 RDL---EEHDQIQTQLEBTPTWIVGALBALKLDE-----KTT----AGDGETPTNL 1144	y	1100 RDL---EEHDQIQTQLEBTPTWIVGALBALKLDE-----KTT----AGDGETPTNL 1144
o	940 HDVLDSKGSKDAEFTIYALLPDGTMKIKWNSKGKLEYEVNDKEFTKTVLAKKVDTGKVDEGT 999	o	940 HDVLDSKGSKDAEFTIYALLPDGTMKIKWNSKGKLEYEVNDKEFTKTVLAKKVDTGKVDEGT 999
y	1145 AFNFDSCEPSHDITSN-----VUNISGNISNISGTVPLGLKRPPDDE 1185	y	1145 AFNFDSCEPSHDITSN-----VUNISGNISNISGTVPLGLKRPPDDE 1185
o	1000 KFTPFAEINYDKDGTMNGKNEIDLKEKSQSLTPKEVPTILSTPQPE 1045	o	1000 KFTPFAEINYDKDGTMNGKNEIDLKEKSQSLTPKEVPTILSTPQPE 1045

STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE  
 MEDIUM TYPE: FILE  
 COMPUTER: IBM PC  
 OPERATING SYSTEM: DOS  
 SOFTWARE: Patent  
 ATTORNEY/AGENT INFORMATION  
 APPLICATION NUMBER:  
 FILING DATE: 01-  
 CLASSIFICATION:  
 TELEPHONE: (703) 633-760-46  
 TELEFAX: (703) 2488505  
 TELEX: 118 LRAYAGVN  
 SEQUENCE CHARACTER:  
 LENGTH: 774 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 633-760-46

RESULTS

19

YNAFRRLTRLTDRLSGLQASHPFAAVAPGVSPQQVWWAVPTLRRDDAGMLKGWSW 634

646 ---LSEA-----THSMALTFDPYSGFCP 666

635 DQALSEALSVASNLLGRSGEPRPRTPHIPLAQPAWAGLLNP 679

GENERAL INFORMATION:

APPLICANT: NIWA, MINBO

APPLICANT: SAITO, YOSHIMASA

APPLICANT: FUJIMURA, TAKAO

APPLICANT: ISHII, YOSHINORI

APPLICANT: NOGUCHI, YUJI

TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS SEE: P.C.

STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ALEXANDRIA

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,760

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 19-929-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 08-633-760-48

Query Match 1.7%; Score 105; DB 1; Length 774;

Best Local Similarity 20.7%; Pred. No. 0..6; Mismatches 241; Indels 242; Gaps 37;

Matches 146; Conservative 76; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARERFGPSRCQGPVVDGAVETTGA--ICTR---LGEPENTILYVVTAL 161

Db 70 LTRRKALGRAEING---AEEAADILVRLGRMVKRRDFALGTBAKD-----M 117

Qy 162 FCAEVEMNVFLHYGLDIDVHGDVTRIPLFQFLMPDYNRLYDFPFTTH---R 216

Db 118 LRAYVAGTNAFLASGA-----PL-PVYEGLGAE---PEPWPHSTAVMR 159

Qy 217 SIGEGFYYTPPYNTGLCHLHDVCVIAFMVALVRVNTAV---ARGAHLAFDENHEG 272

Db 160 RLG-----LNGSFTFLWMLAIFVVGANALKRYDGGRD 197

Qy 273 AV-LPPDITYTYFQSSSSGTTARGARRNDVNSTSKEPSGCFER-----RLAS--IM 322

Db 198 LICIPGAEDRDEADLTLRPAVDALLKAMGDSADAGGSNNWAVAPGRTAIGRIL 257

RESULTS

19

Qy 323 AADFLAHAEVFTNGTGYETPTTIKENMFIGNEGTIPRLNALGSYTVARVAGTIGANVFS 382

Db 258 AGDPHRVFEI---PGIYAGHHIACDRFM-1G---TYP-----AKDGGGPSPFNRF 412

Qy 383 PNSA-----LYLTEVEDSGMTE-----

Db 299 HNGKVAYCATHAFNDINDHILYEQFAGEERTGARNDPVAWDRDFAVGGDADREFD 358

Qy 413 YQFAGPHLANNPQDROGHVLSOSTGSNTESVYDIALICSGAPILLFLYFLRC 472

Db 359 KTRIGGPVITAGDP---RDGALTLRSVOPAETDLSFDCLTRMP---GASTVADLY----D 407

Qy 473 AGATPG---SH---GDALKYVTFDSEFPCSLCEKHPVCAHTTWRRL---DRMP 521

Db 408 ATRGWGLIDHNLVYGDVAGSIGHLVRAVPSRPRENGMLPVPGWSGEHEWRGWIHPAMP 467

Qy 522 RFQQATRQPIGVFGFTMNSCY-----SDCDPLNRYAPY-----LILRKPGDGTB 564

Qy 520 DAAAIHADTLSP---HVGLLRRLAIGARDSSAEGRLMVLVANDGRMDAESA/ASA 574

Db 468 R---VIDPFGGIIVTANRNVVADDHPDLYCTDHP---PRAERIMKRLVANPAFAVD 519

Qy 565 AAXATMMDTYRATLERLFDLEQERLDRGA---PCSSRGLSSVIV-----D 608

Qy 609 HPTPRRLDTL---RARIQOTTO-----FMKVJLVETRDVKIREG--- 645

Db 575 YNAFRAALTRLTVTDTSQLEQAISHPRAAVAPGVSPQGQWWA/PTLRLDDAGMLKGMSW 634

Qy 646 ---LSEA-----THSMALTFDPSGARCP 666

Qy 635 DQALSEALSVASNLLGRSGEHRPRTPHIPLAQPAWAGLLNP 679

RESULTS

20

US 08-931-608A-5

; Sequence 5, Application US/08931608A

; Patent No. 6302685

; GENERAL INFORMATION:

; APPLICANT: Lobel, Peter

; APPLICANT: Sleat, David E.

; TITLE OF INVENTION: HUMAN LYOSOMAL PROTEIN AND METHODS OF ITS USE

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/931,608A

ATTORNEY/AGENT INFORMATION:

NAME: Lobel, Peter

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 19-929-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 08-931-608A-5

Query Match 1.7%; Score 105; DB 1; Length 774;

Best Local Similarity 20.7%; Pred. No. 0..6; Mismatches 241; Indels 242; Gaps 37;

Matches 146; Conservative 76; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAARERFGPSRCQGPVVDGAVETTGA--ICTR---LGEPENTILYVVTAL 161

Db 70 LTRRKALGRAEING---AEEAADILVRLGRMVKRRDFALGTBAKD-----M 117

Qy 162 FCAEVEMNVFLHYGLDIDVHGDVTRIPLFQFLMPDYNRLYDFPFTTH---R 216

Db 118 LRAYVAGTNAFLASGA-----PL-PVYEGLGAE---PEPWPHSTAVMR 159

Qy 217 SIGEGFYYTPPYNTGLCHLHDVCVIAFMVALVRVNTAV---ARGAHLAFDENHEG 272

Db 160 RLG-----LNGSFTFLWMLAIFVVGANALKRYDGGRD 197

Qy 273 AV-LPPDITYTYFQSSSSGTTARGARRNDVNSTSKEPSGCFER-----RLAS--IM 322

Db 198 LICIPGAEDRDEADLTLRPAVDALLKAMGDSADAGGSNNWAVAPGRTAIGRIL 257

RESULTS

21

Qy 323 AADFLAHAEVFTNGTGYETPTTIKENMFIGNEGTIPRLNALGSYTVARVAGTIGANVFS 382

Db 258 AGDPHRVFEI---PGIYAGHHIACDRFM-1G---TYP-----AKDGGGPSPFNRF 412

Qy 383 PNSA-----LYLTEVEDSGMTE-----

Db 299 HNGKVAYCATHAFNDINDHILYEQFAGEERTGARNDPVAWDRDFAVGGDADREFD 358

Qy 413 YQFAGPHLANNPQDROGHVLSOSTGSNTESVYDIALICSGAPILLFLYFLRC 472

Db 359 KTRIGGPVITAGDP---RDGALTLRSVOPAETDLSFDCLTRMP---GASTVADLY----D 407

Qy 473 AGATPG---SH---GDALKYVTFDSEFPCSLCEKHPVCAHTTWRRL---DRMP 521

Db 408 ATRGWGLIDHNLVYGDVAGSIGHLVRAVPSRPRENGMLPVPGWSGEHEWRGWIHPAMP 467

Qy 522 RFQQATRQPIGVFGFTMNSCY-----SDCDPLNRYAPY-----LILRKPGDGTB 564

Qy 520 DAAAIHADTLSP---HVGLLRRLAIGARDSSAEGRLMVLVANDGRMDAESA/ASA 574

Db 468 R---VIDPFGGIIVTANRNVVADDHPDLYCTDHP---PRAERIMKRLVANPAFAVD 519

Qy 565 AAXATMMDTYRATLERLFDLEQERLDRGA---PCSSRGLSSVIV-----D 608

Qy 609 HPTPRRLDTL---RARIQOTTO-----FMKVJLVETRDVKIREG--- 645

Db 575 YNAFRAALTRLTVTDTSQLEQAISHPRAAVAPGVSPQGQWWA/PTLRLDDAGMLKGMSW 634

Qy 646 ---LSEA-----THSMALTFDPSGARCP 666

Qy 635 DQALSEALSVASNLLGRSGEHRPRTPHIPLAQPAWAGLLNP 679

RESULTS

22

US 08-931-608A-5

; Sequence 5, Application US/08931608A

; Patent No. 6302685

; GENERAL INFORMATION:

; APPLICANT: Lobel, Peter

; APPLICANT: Sleat, David E.

; TITLE OF INVENTION: NOVEL HUMAN LYOSOMAL PROTEIN AND METHODS OF ITS USE

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/931,608A

ATTORNEY/AGENT INFORMATION:

NAME: Jackson, Esq., David A.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 601-1-077

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 635 amino acids

TYPE: amino acid

STRANDDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-08-931-608A-5

Query Match 1.7%; Score 104.5; DB 4; Length 635;  
Best Local Similarity 21.0%; Pred. No. 0.47;  
Matches 77; Conservative 36; Mismatches 121; Indels 133; Gaps 14;

Qy 245 MAVAFLRVNNTAVARGAAHLAFAFDENH-EGAVLPFDITYFQOSSSGCTTARGARRNDVN 303  
Db 10 VAIAMSSIAHED---AWSTHTQAMSPDASTOVLAASTSATTTGNA--YTLN 62

Qy 304 STSKPSPSGFERLALASIAADTALHAEVNTGIVYESTPTDIKEWPMFIGMEGTIPRLN 363  
Db 63 MTGSPRIDA---AVTALADPHLYEVALK-----DRNPD 95

Qy 364 ALGSYTAVGIVGAMVESPNSALYLTVEVDGSMTEAKDGGPQSFNRFYQAGPHILAN 423  
Db 96 ALQFLAGYT---TGSALFGKPLTPSQTET-----RF----GP-----127

Qy 424 PQTDRGHVLSSQGTGSSNTTFSYDYLALICGFAPIALARLLFYLERCDAGAFTGGHDDA 483  
Db 128 TQSQDAVVAHLQAOQFINNEVAPNRL-LISADGT----AGAATNGFRTS 172

Qy 484 LKYYTGTFDSEIPCSLCXTRPVCAHTTVHLRQRMRMFRGQATRQPIGVFGTMNSQYSD 543  
Db 173 IK-----RPSANGR-----181

Qy 544 CDPLGNAYAPYLILRKPGDQEAAKATMDTYRATLERLFDQERLLIDRGAPCSBGLS 603  
Db 182 -EFFPANDAPALVPSLGDSDNAVGLQNYSVKHTLHHVY--HPEDVTVGPNVGTQAAA 237

Qy 604 SVTIDHP 610  
Db 238 AVAAHHP 244

RESULT 21

US-09-851-847-5

Sequence 5, Application US/09851847  
Patent No. 6638712

GENERAL INFORMATION:  
APPLICANT: Lohel, Peter  
Sriet, David E.

TITLE OF INVENTION: NOVEL HUMAN LYOSOMAL PROTEIN AND METHODS OF ITS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/851,847  
FILING DATE: 09-May-2001  
PRIORITY CLASSIFICATION: <Unknown>  
APPLICATION NUMBER: 08/931,608  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson, Esq., David A.

REGISTRATION NUMBER: 26,742  
REFERENCE DOCKET NUMBER: 601-1-077  
TELECOMMUNICATION INFORMATION:  
PHONE: 011-47-5800  
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:

LENGTH: 635 amino acids  
TYPE: amino acid  
STRANDBNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-851-847-5

Query Match 1.7%; Score 104.5; DB 4; Length 635;  
Best Local Similarity 21.0%; Pred. No. 0.47;  
Matches 77; Conservative 36; Mismatches 121; Indels 133; Gaps 14;

Qy 245 MAVAFLRVNNTAVARGAAHLAFAFDENH-EGAVLPFDITYFQOSSSGCTTARGARRNDVN 303  
Db 10 VAIAMSSIAHED---AWSTHTQAMSPDASTOVLAASTSATTTGNA--YTLN 62

Qy 304 STSKPSPSGFERLALASIAADTALHAEVNTGIVYESTPTDIKEWPMFIGMEGTIPRLN 363  
Db 63 MTGSPRIDA---AVTALADPHLYEVALK-----DRNPD 95

Qy 364 ALGSYTAVGIVGAMVESPNSALYLTVEVDGSMTEAKDGGPQSFNRFYQAGPHILAN 423  
Db 96 ALQFLAGYT---TGSALFGKPLTPSQTET-----RF----GP-----127

Qy 424 PQTDRGHVLSSQGTGSSNTTFSYDYLALICGFAPIALARLLFYLERCDAGAFTGGHDDA 483  
Db 128 TQSQDAVVAHLQAOQFINNEVAPNRL-LISADGT----AGAATNGFRTS 172

Qy 484 LKYYTGTFDSEIPCSLCXTRPVCAHTTVHLRQRMRMFRGQATRQPIGVFGTMNSQYSD 543  
Db 173 IK-----RPSANGR-----181

Qy 544 CDPLGNAYAPYLILRKPGDQEAAKATMDTYRATLERLFDQERLLIDRGAPCSBGLS 603  
Db 182 -EFFPANDAPALVPSLGDSDNAVGLQNYSVKHTLHHVY--HPEDVTVGPNVGTQAAA 237

RESULT 22

US-08-019-870-5

Sequence 5, Application US/08019870  
Patent No. 5336613

GENERAL INFORMATION:  
APPLICANT: NIWA, MINEO  
APPLICANT: YOSHIMASA, SAIKO  
APPLICANT: SASAKI, HITOHI  
APPLICANT: ISHII, YOSHINORI  
TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OELON, SPIRAK, McCLELLAND, MAIER & NEUSTADT,  
CITY: OELON  
STATE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/851,847  
FILING DATE: 09-May-2001  
PRIORITY CLASSIFICATION: <Unknown>  
APPLICATION NUMBER: 08/931,608  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson, Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE DOCKET NUMBER: 601-1-077  
TELECOMMUNICATION INFORMATION:  
PHONE: 011-47-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: 18-791-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-019-870-5

Query Match 1.7%; Score 104.5; DB 1; Length 774;  
 Best Local Similarity 21.7%; Prod. No. 0.68;  
 Matches 91; Conservative 41; Mismatches 136; Indels 151; Gaps 19;  
 QY 372 VAGVIGAMWFSPPNSA-----LYTTEVEDOSGMTE-----AK 401  
 Db 288 VPGVPGFPFAHNGKVAFCVTHAFMDIHDLYLEFAGEGRTARFGRDNDFEPPAWSRDRIAV 347  
 QY 402 DGGGPFSFTRFYQFAGPHLAANPOTDRDGHVLSSQSTSNTFSDYLA-----LI 453  
 Db 348 RGGADRFREDFIVETPHGPVAGDP--RGGAAITLRSVQFAETDLSFDCLTRMPGASHNLV 404  
 QY 454 CGFEGAPLLARLLFYLERCDAGAFTGGHGDALKYVGTGFD-SE1PCSLCEKTRPYCAHT 512  
 Db 405 AGDVGASIGSHLVTAQLYDA---TRG-----WGLIDRARVPSRDRPENGMLPVPGWSG 453  
 QY 513 VHRRL---QRMFRGQITRQFPGVFGTMNSQY-----SPCDPLGNYAPY--- 553  
 Db 454 EHEWRGWIHEAMR---VTDPPGQIIVTANVRVADDHPDYLCTDCHP---PYRAER 505  
 QY 554 ---LILRKGDQTEAAKATMDTIVRATLERFLDQEQLRLLRGAA-PCSSCGLSSVY- 607  
 Db 506 IMKRLVANFAFAVDDAAAHADTLSP----HYGLLRLRLEAIGARDSSAAGLROMLVA 560  
 QY 608 -----DHPTRFLRDLT---FARIEOTTO-----FMKVL 634  
 Db 561 WDGRMDAASEVASYAAYNAFRAALRPLVTDGQLEAISHPEAAVPGVSPQQQWVWAAPTL 620  
 QY 635 VETRYKIREG-----LSEA-----THSMALTFDPYSGAACP 666  
 Db 621 LRDDDAGMKGWSWDQALSEALSVASQNLTGRSMGEERPRFTPLATQFPAWAGLNP 679  
 QY 624 ---EQTITQFMKVLYVETRDYKIR-EGL-----SEATHSMALTEDPY-SGAGCPITN 669  
 Db 606 MHKRERTCKDYKIAVETVNDLRLPBALESWKDMDATEQVHTATMLDVLBEGAFLLADN 665  
 QY 670 -----FLVGRTHLAV-----VODIALSQQCHCVFVQGQQVGEGRNFR- NQFOPVLRR 712  
 Db 666 VREPARPLAAQNVVLETVLSTEGQVQELVFPQEYASSESSIOLSANTIKONSRRNGVVKV 725  
 QY 713 RFDVLPN---GGF1STRSITYVTL---SEGIVPSAAPTILQO-----DAPAGRTPPDGLA 759  
 Db 726 VPI-LNNNLGLFLSINATVKGAEZGTGGPGGASUVNSQVIAASSINKESSRVP--LM 781  
 QY 760 RVSVEVIRDYKVNRYVFSGNCT- NLSE 786  
 Db 782 DPVIFTVAHLERKHN--FNANCSFWNTSE 808

RESULT 24  
 US-08-019-870-3  
 ; Sequence 3, Application US/08019870  
 ; Patent No. 533613  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Petrenko, Alexandre  
 ; TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF ALPHA-LATROTOXIN,  
 ; FILE REFERENCE: 1049-1-007  
 ; CURRENT APPLICATION NUMBER: US/08/811,519B  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 1  
 ; LENGTH: 1471  
 ; TYPE: PR  
 ; ORGANISM: rat  
 US-08-019-519-1

Query Match 1.7%; Score 104.5; DB 4; Length 1471;  
 Best Local Similarity 19.6%; Prod. No. 2.3; Mismatches 98; Indels 339; Gaps 47;  
 Matches 182; Conservative 98; Nucleotides 310; Score 128  
 Qy 73 LAGAGITLKLUTSHFVPSVVFHGGKXVLPSSAAAPNLTRACNAARERFESR---CCGP 128  
 Db 4 LAAAGAGLCTT-----VIVTASATGSLR---AGLPGMRRFLACEY 44

RESULT 24  
 US-08-019-870-3  
 ; Sequence 3, Application US/08019870  
 ; Patent No. 533613  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NIWA, MINEO  
 ; APPLICANT: YOSHIMASA, SAITO  
 ; APPLICANT: Sasaki, Hitoshi  
 ; APPLICANT: ISHII, YOSHINORI  
 ; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESS: P.C.  
 STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Parent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICANT: US/08/019,870  
 FILING DATE: 19930219  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Oblon, No. 531661 man F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 18-791-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-019-870-3

Query Match 1.6%; Score 103; DB 1; Length 774;  
 Best Local Similarity 20.5%; Pred. No. 0.97; Mismatches 80; Indels 226; Gaps 37;  
 Matches 143; Conservative 80; Mismatches 248; Indels 226; Gaps 37;

Qy 109 LTR--ACNARERGFSRCCGPPGAVETGAS--ICTR---LGLEPENTILYLVITAL 161  
 Db 70 LTRKALGRAEWLG--AEEAADILVRLGKVRDRFEALGVRAKD----M 117  
 Qy 162 FKEAVFMCVFLHYGGLDIVHNGDVIRLPIFLVQLMMPDYNRPPFNTHE----R 216  
 Db 118 LRAYAGVNFNLASGA----PL-FEVYGLGAE--FDPWEPWHSIAWR 159  
 Qy 217 SIGGCFVYPFPYNTGLCHIHDCTVIAPMAYALRVNNTAV----ARGAHAFLDENHEG 272  
 Db 160 RLG-----LLMSWVFLWMLALPVGAANALKRYDDGGRD 197  
 Qy 273 AV-LPFDITYFQSSSGTTTARGRNDVNTSKPSBSGGER----PLAS---IM 322  
 Db 198 LLCPPGAENDRLEADLAVTRPAVDALLKMGCGDASDAAGGGSNWAVGRTATGRPL 257  
 Qy 323 AADTLAHAEVTFNTGTYEEPTDKWPMFIMGEGTLPLNALGSYTAvgVIGANVFS 382  
 Db 258 AGDPRVFEI--POMYAQHHLAIDRFM-IGL-TYPCPGFPHAH----GKvAYS 306  
 Qy 383 PNSA-----LYLPEVEDSGMTE-----AKDGGPSPFNRFYQFAGHL 420  
 Db 307 VTHAFMDIHDLYLEQFAGERTRTARFGNDTPEPVMSRDRRAVRGADRFIVTRHGPVI 366  
 Qy 421 RANPQTDGRHVLSSQSTGSSNTFSVYDALLICGFGAPILLARLFYLERCDAGAFTG-- 478  
 Db 367 AGDP---RDAHLTRSVQQAETDLSFDCTTRMP--GASTVQLY----DTRGWLII 415  
 Qy 479 GH---GDAKXYTGTGDFSEIPSCSCEKHTRPVCAHTYVHLR----QRMPPFGQATRQ 529  
 Db 416 DHNLVAGDVAASGHILVRAVPSRGPNGFLPVPGWSGHEMGWPHAMPR--VIDP 472  
 Qy 530 PIGVFTMNRY-----SDCDPLGNYAP-----LIRKPGDQEAKATMQD 572  
 Db 473 PGGIITVANNRVVADHPDYLCTDCHP---PRAERIMKRLVANPAVDDAAATHAD 527  
 Qy 573 TYRATLRLFIDLEOERLDRGA - PCSSIGLSSVIV-----DHSPTFRRL 616

RESULT 25  
 US-08-633-760-44  
 Sequence 44, Application US/08633760  
 Patent No. 5804429  
 GENERAL INFORMATION:  
 APPLICANT: NIWA, MINEO  
 APPLICANT: SAITO, YOSHIMASA  
 APPLICANT: FUJIMURA, TAKAO  
 APPLICANT: ISHII, YOSHINORI  
 APPLICANT: NOGUCHI, YUJI  
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE  
 NUMBER OF SEQUENCES: 64  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESSEE: P.C.  
 STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400  
 CITY: ARLINGTON  
 STATE: VIRGINIA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/633,760  
 FILING DATE: 01-MAY-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 18-929-0 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2200  
 INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-633-760-44

Query Match 1.6%; Score 103; DB 1; Length 774;  
 Best Local Similarity 20.6%; Pred. No. 0.97; Mismatches 77; Indels 242; Gaps 37;  
 Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR--ACNAAARRERGFSRCCGPPGAVETGAS--ICTR---LGLEPENTILYLVITAL 161  
 Db 70 LTRKALGRAAWLG--AEEAADILVRLGKVRDRFEALGVRAKD----M 117  
 Qy 162 FKEAVFMCVFLHYGGLDIVHNGDVIRLPIFLVQLMMPDYNRPPFNTHE----R 216  
 Db 118 LRAYAGVNFNLASGA----PL-FEVYGLGAE--FDPWEPWHSIAWR 159  
 Qy 217 SIGGCFVYPFPYNTGLCHIHDCTVIAPMAYALRVNNTAV----ARGAHLAFLDENHEG 272  
 Db 160 RLG-----LLMSWVFLWMLALPVGAANALKRYDDGGRD 197  
 Qy 273 AV-LPFDITYFQSSSGTTTARGRNDVNTSKPSBSGGER----PLAS---IM 322  
 Db 198 LLCPPGAENDRLEADLAVTRPAVDALLKMGCGDASDAAGGGSNWAVGRTATGRPL 257  
 Qy 323 AADTLAHAEVTFNTGTYEEPTDKWPMFIMGEGTLPLNALGSYTAvgVIGANVFS 382  
 Db 258 AGDPRVFEI--POMYAQHHLAIDRFM-IGL-TYPCPGFPHAH----GKvAYS 306  
 Qy 383 PNSA-----LYLPEVEDSGMTE-----AKDGGPSPFNRFYQFAGHL 420  
 Db 307 VTHAFMDIHDLYLEQFAGERTRTARFGNDTPEPVMSRDRRAVRGADRFIVTRHGPVI 366  
 Qy 421 RANPQTDGRHVLSSQSTGSSNTFSVYDALLICGFGAPILLARLFYLERCDAGAFTG-- 478  
 Db 367 AGDP---RDAHLTRSVQQAETDLSFDCTTRMP--GASTVQLY----DTRGWLII 415  
 Qy 479 GH---GDAKXYTGTGDFSEIPSCSCEKHTRPVCAHTYVHLR----QRMPPFGQATRQ 529  
 Db 416 DHNLVAGDVAASGHILVRAVPSRGPNGFLPVPGWSGHEMGWPHAMPR--VIDP 472  
 Qy 530 PIGVFTMNRY-----SDCDPLGNYAP-----LIRKPGDQEAKATMQD 572  
 Db 473 PGGIITVANNRVVADHPDYLCTDCHP---PRAERIMKRLVANPAVDDAAATHAD 527  
 Db 528 TLSP---HVGLIERRLEBLAGGDDSAEGLRNLVAVDGRMDAASEVAYNAFRAL 582  
 Qy 617 DTL---RARLEQTTO-----FMKVLYETRDYKIREG----LSEA- 649  
 Db 583 TRLYTDTSQGEQAIHSPFARAVPGVSQGQYWWAVPTLRRDDAGMLKERSWDQALSEAL 642

Qy 273 AV LPDDITYTQFQSSSSGTTARGARRNDVNSTSKPSGGFER-----RIAS---IM 322  
 Db 198 LCLCIPGAEDRLEADLTLRPAVDLKKANGCDAASDAGGSNNWAVAPERTATGRPL 257  
 Qy 323 AADTLHDEVINNTGIVEETPDIKEMPFIIGEETLPRNALGSYTARYAVIGAMVFS 382  
 Db 258 AGPDPHRYFEI---PGYAAQHIACDRDM---ISU---TYP---GVPEPFPHF 298  
 Qy 383 PNSA-----LYLTIVEDSGME-----AKDGPGEFNR 412  
 Db 299 HNGKUAVCVTHAAMDIDLYLQFAGGCRTRAFGNDPEPWAWSRDRIAVRGGADREFIV 358  
 Qy 413 YQFAGPHIAANPQTDRGHVLSSOSTGSNTFSVDYLALICFGAPLLARLFYLERCD 472  
 Db 359 ETHMGPVIAQDP---RDEAALTLSRVOPEATDJSFDLTMRP---GASTVADY---D 407  
 Qy 473 AGAFTG---GH---GDALKYVGTGTEDEBIPCSLCEKHTRPVAHTTIVHRLR---QRMP 521  
 Db 408 ATRCWGLIDHNLVAGDVSIGHLVRGVPSSRRENWLPGVGSHEWNGWIPHEAMP 467  
 Qy 522 RFGQATRQPIGVGFTGMSQY-----SDCDPLGMNAPY-----LLRKPGDQTE 564  
 Db 468 R---VIDPFGIIYTANRVRVADDHPDYLCTDCHP---PRAERIMKRLVANPAFAVD 519  
 Qy 565 AAKATMDQTYRATERLFLDQEPLRLLGA---PCSSRGFLSSVIV-----D 608  
 Db 520 DAAIMHADLSP---HYGLLARRLEAGLARDSSAAEGLRQMLVANDGRMDAASEVASA 574  
 Qy 609 HPTFRLDFTL---RARIEQTTO-----FMKVLYVETRDYKIREG--- 645  
 Db 575 YNAPRRAUTRLVTDTRSLGQLAISHPFAAVAPGVSQPGQWVWAPTLRDDAGMLKGWSW 634  
 Qy 646 ---LSEA-----THSMALTFDPYSGAFCP 666  
 Db 635 DQALSEALSVASQNLTRGSGWGBHRRPRTFHPLATQFPAWAGLNP 679

RESULT 27  
 US-08-070-165F-6  
 ; Sequence 6, Application US/08070165F  
 ; Patent No. 5750355

GENERAL INFORMATION:  
 ; APPLICANT: Chiu, Ing-Ming  
 ; APPLICANT: Poulin, Matthew L  
 ; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Ing-Ming Chiu  
 ; STREET: S2012 Davis Medical Research Center, 480 West  
 ; CITY: 9th Avenue  
 ; STATE: Columbus  
 ; ZIP: 43210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/070,165F  
 ; FILING DATE:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (614) 293-8093  
 ; TELEFAX: (614) 293-5611  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 729 amino acids  
 ; TOPOLogy: linear  
 ; MOLECULE TYPE: protein

US-08-070-165F-6

Query Match 1.6%; Score 103; DB 4; Length 3472;  
 Best Local Similarity 20.2%; Pred. No. 16; Mismatches 175; Indels 160; Gaps 24;  
 Matches 98; Conservative 98; Organism: Cenarchaeum symbiosum

Qy 82 LTTSHFYPSPVVFHGKHTVLEPSSAAPNLTRACNAARERRGFSRQGPPVFDGAVETTGAEI 141  
 Db 928 LAVSGYAEPISVVP---GRHAPVGAAGTFSQSIGNATELYG---S1PNPTIDFGTTLTGA--- 981  
 Qy 142 CTRLGHEPENTILYLVVTLALFKEAEMCNVFLHY---CGGLDIAVHNGDVTRIPLEPV 196  
 Qy 982 ---AFSADGTVFVFLSDGPGRVVPYSNLPDISSAAAGGFTVPGVSDI----- 1029  
 Db 197 QLFMPD-VNRLVPPDENTHRSIIGEG-FVYPTPPYNTGILCHLTHDCVIAPMAMAVALYRN 254

Query Match 1.6%; Score 102; DB 1; Length 729;  
 Best Local Similarity 20.0%; Pred. No. 1.1; Mismatches 69; Conservative 69; Indels 168; Gaps 26;  
 Matches 111; Organism: Cenarchaeum symbiosum

Qy 355 MEGTLPILNALGSYTARVAGYIGMVFSPNSALYLTVEEDS-----GMTEAKDG 403  
 Db 128 MESSVP---SDEGNYTCIMENYGSI---NETYHLDVVERSPHRPLQAGLPANTTKVG 181

Qy 404 GPGSPFNRFYQFAGPHL-----AANPQTDRDGH-----VLSQSTGSSNTESVYDYLAL 452

Query Match 1.6%; Score 102; DB 2; Length 729;  
 Best Local Similarity 20.0%; Pred. No. 1.1;  
 Matches 69; Mismatches 206; Indels 168; Gaps 26;

355 MEGTIPRLNALGSYTAARVAGVIGAWFSPNSALYTEVEDS-----GMTEAKDG 403  
 182 GDAEFVCKVYSDAQPHICWIRHPELNGSKIGPDGHPLKVLKAAGYNTIEKEIYVRN 241  
 453 ICGFQAPLARLFLYLERDAGAFT--GGHGDALKYVTGTF----DSEIPCS----- 498  
 242 VS-----FE-DAGEYTCAGNSTGISTHAWTLVLPDEERLDSSSEYTEI 286  
 499 -----LCEKHTRFC-----AHTYVHLRQLRQMPRFQGOAT----- 527  
 287 AIVCGGGFLITCMIGTIVCMKGRGKSDFESSPVAHFLSKSLPLRQTVSADSSSM 346  
 528 -----RQPIGFGTMNSQYSDCDPLGNYA-----LILRKP-GD----- 561  
 347 NSNTPLVKTTRLSSNNTHILAGVSEELPBDPKWYPREKLTKPLGQGCQVWNA 406  
 562 -----QTEAKATQDTYRATLERFLIDQEBLLDR-----GAPCSSE 600  
 407 EAVGIDKDRPKDAATAVTMLKDATERDLSLVSNEMMKIGKHKNINLGA-CTOD 465  
 601 GLSSVTVCHPT--ERRLDLTARLISQTTQFMKVLYETDVKIREGLESATHSMALTF 657  
 466 GPVIVVYASKGNLREYLRTPQGNSYEDINRPEEQNTFK--DLYSCTYQOLARM 522  
 658 DPYSGAPFC----PITNELVKRTHLAVYQDALSQ--CHCVYQQVEGNGFRNQFQPYL 710  
 523 EYLASKQKTHDLAARNVLYTEINVMKIADEGLARDINNTDYKKUTN3R-----LPYK 576  
 711 RRFEDVLNGGF1STRSTTVLUSGPVSPASAPNTLGDQDAPARTFDDLARVSV-EVIRDI 769  
 577 WMAPEALLDRVTHOSD--WSEFGVLMWEITLG---GSPYPS---IPVEBLFKL 624  
 707 RVENRVRVPSGNCTN 783  
 625 KEGRHMDKPGNCTN 638

RESULT 28  
 US-08-895-418-6  
 Sequence 6, Application US/0885418  
 Patent No. 592528  
 GENERAL INFORMATION:  
 APPLICANT: Chiu, Ing-Ming  
 TITLE OF INVENTION: Native Fibroblast Growth Factor (aFGF)  
 NUMBER OF SEQUENCES: 12

ADDRESSEE: Poulin, Matthew L  
 STREET: S2052 Davis Medical Research Center, 480 West  
 STREET: 9th Avenue  
 CITY: Columbus  
 STATE: Ohio  
 COUNTY: USA  
 ZIP: 43210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOO/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-885,418  
 FILING DATE:  
 CLASSIFICATION: 435  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (614)-293-8093  
 TELEFAX: (614)-293-5631  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 729 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-885-418-6

Query Match 1.6%; Score 102; DB 2; Length 729;  
 Best Local Similarity 20.0%; Pred. No. 1.1;  
 Matches 69; Mismatches 206; Indels 168; Gaps 26;

QY : 355 MEGTIPRLNALGSYTAARVAGVIGAWFSPNSALYTEVEDS-----GMTEAKDG 403  
 QY : 182 MBSVVP-SDENYNTCIMENEGSI----NHTYHIDUVVERSSPHRLQAGLPANTTIVKG 181  
 QY : 404 GPGSPFARFYQAGPHL----AANPQDFDRGHH----VLSQSTGSNTESFYLYAL 452  
 QY : 182 GDAEFVCKVYSDAQPHQWIRHPELNGSKIGPDGHPLKVLKAAGVNTTKEIEVLYVRN 241  
 QY : 453 ICGFQAPLARLFLYLERDAGAFT--GGHGDALKYVTGTF----DSEIPCS----- 498  
 QY : 242 VS-----FBS-DAGEYTCAGNSTGISTHAWTLVLPDEERLDSSSEYTEI 286  
 QY : 499 -----LCEKHTRFC-----AHTYVHLRQLRQMPRFQGOAT----- 527  
 QY : 287 AIVCGGGFLITCMIGTIVCMKGRGKSDFSSPAVHKLSKSLPLRQTVSADSSSM 346  
 QY : 528 --RQPIGFGTMNSQYSDCDPLGNYA-----LILRKP-GD----- 561  
 QY : 347 NSNTPLVKTTRLSSNNTHILAGVSEELPBDPKWYPREKLTKPLGQGCQVWNA 406  
 QY : 562 -----QTEAKATQDTYRATLERFLIDQEBLLDR-----GAPCSSE 600  
 QY : 601 GLSSVTVCHPT--ERRLDLTARLISQTTQFMKVLYETDVKIREGLESATHSMALTF 657  
 QY : 466 GPVIVVYASKGNLREYLRTPQGNSYEDINRPEEQNTFK--DLYSCTYQOLARM 522  
 QY : 658 DPYSGAPFC----PITNELVKRTHLAVYQDALSQ--CHCVYQQVEGNGFRNQFQPYL 710  
 QY : 523 EYLASKQKTHDLAARNVLYTEINVMKIADEGLARDINNTDYKKUTN3R-----LPYK 576  
 QY : 711 RRFEDVLNGGF1STRSTTVLUSGPVSPASAPNTLGDQDAPARTFDDLARVSV-EVIRDI 769  
 QY : 625 KEGRHMDKPGNCTN 638

RESULT 29  
 US-07-747-901A-3  
 Sequence 3, Application US/07747901A  
 ; Sequence 3, Application US/07747901A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Iwami, Morita  
 ; APPLICANT: Aramori, Ichiro  
 ; APPLICANT: Fukagawa, Masao  
 ; APPLICANT: Isogai, Takao  
 ; APPLICANT: Kojo, Hitoshi  
 ; TITLE OF INVENTION: CEPHALOSPORIN C ACYLASE  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESS: P.C.  
 ; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOO/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07-747,901A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (614)-293-8093  
 ; TELEFAX: (614)-293-5631  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 729 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/747,901A  
 FILING DATE: 19910820  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Obion, No. 5192678man F.  
 REGISTRATION NUMBER: 24, 618  
 REFERENCE/DOCKET NUMBER: 18-709-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 521-4500  
 TELEFAX: (703) 486-3347  
 TELEX: 244855 OPAT UR

SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein

US-07-747-904-A3

Query Match 1.6%; Score 102; DB 1; Length 774;  
 Best Local Similarity 20.6%; Pred. No. 1.2;  
 Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR- ACNAARBERGFSSRGQPPYDGAETTGGAE-ICTR---LGLEPENTILLYVTTAL 161  
 Db 70 LTRRKALGRRAEWLG- -EEAAEADILYLRLGKVERDFEALGVPEAKD-----M 117

Qy 162 FKEAVFMCNVFLHYGLDVHNGDVIRIPLPQVQLEMPDVNRLVPDPFENTH---R 216  
 Db 118 LRAYAGVNAFLAGA---PL PVEYGLGAE---PEPWEPHSLAVMR 159

Qy 217 SIGEFPVYPTPFPYNTGLCHLHDCVIAPIAVLVRVNTAV---ARGAAHIAFDENHEG 272  
 Db 160 RLG-----LLMGSVWPKLWRMLALPVGAANALKURYDDGGRD 197

Qy 273 AV-IPFDITYTYFQSSSSCTTARGARRDNDVNSTSKPSSQGPYFPER---RLAS---IM 322  
 Db 198 LLCPGGAADRLEADLTLRPAVDALLKAMGDASDAGGGNNNWAAPGRBTATGRPL 257

Qy 323 AADTAHALHAYVINTGIVYEETPTDIKEWPKMFIGEKGTLPLRNLALGSSYTTARVAGVGMVFS 382  
 Db 258 AGDPHRVFEI---PSMYAQHHLACDRFDN-IGL---TVP-----GPGFPHFA 298

Qy 383 PNSA-----IYLTEVEDSGTE-----AKDGGGPSPENRP 412  
 Db 299 HNGKVAYCITHAFMDIHDLYLEQPAGEGTTARFGNDFFPVAWSRDRTAVRGGADREDDIV 358

Qy 413 YQFASPHLLANPOTRDGIVLSSGSGNTNTFSDVYLALLCGFAPLARLFLYERCD 472  
 Db 359 ETRHGPVIAQDP---RDGAHTLRSQFETDLSFDCLTRMP---GASTVAGLY---D 407

Qy 473 AGAFTG- -GH---GDAKLYVUTGTGFEDSEIPLCSLCEKHTRPAVCAHTVHLR-----ORMP 521  
 Db 408 ATRGGLILIDNLVAEDVASSIGHLYRARVSPRENGWAVPVCWSGEHEWGRPHAMP 467

Qy 522 RFGQATRQPLGVFTGMNSQY-----SDCDPLGMNAY-----LILRKPGDQTE 564  
 Db 468 R---VTDPPGQGIVTANNNYVADDPFDYCTDCHP---PYAERBRMKRVLVANPAPAVD 519

Qy 565 AAKATMQDTKTRATLRLFELQEBILLDQA---PCSSSGLSSSTV-----D 608  
 Db 520 DAAATHADLTLSP-----HYGDLRRLREALGARDSSAEEGRMLVANDGRMDAASEVASA 574

Qy 609 HPTPRILDTD---RARIEQTTQ-----FNUKVIVETRDYKIREG--- 645  
 Db 575 YNAPRPLAHTLVLTPSGLEPAISHPAAVARYGVSPOQGVWAWPTLRLDDAGMLKCNWSW 634

Qy 646 ---LSEA-----THSMALTFDPYSGAFCP 666  
 Db 635 DQALSEALSVASQNLTGRIWGEHHRPFTPLATOQFPAWGLLNP 679

GENERAL INFORMATION:  
 APPLICANT: Iwami, Morita  
 APPLICANT: Aramori, Ichiro  
 APPLICANT: Fukagawa, Masao  
 APPLICANT: Isogai, Takao  
 APPLICANT: Kojo, Hitoshi  
 TITLE OF INVENTION: CEPHALOSPORIN C ACYLASE

NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESSE: P.C.  
 STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 CITY: Arlington  
 STATE: Virginia  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/935, 312  
 FILING DATE: 19920826  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Obion, No. 5320946man F.  
 REGISTRATION NUMBER: 24, 618  
 REFERENCE/DOCKET NUMBER: 18-769-0 DIV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 486-1500  
 TELEFAX: (703) 486-2347  
 TELEX: 248955 OBAT US  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-07-935-312-3

Query Match 20.6%; Score 102; DB 1; Length 774;  
 Best Local Similarity 20.6%; Pred. No. 1.2;  
 Matches 145; Conservative 77; Mismatches 241; Indels 242; Gaps 37;

Qy 109 LTR- ACNAARBERGFSSRGQPPYDGAETTGGAE-ICTR---LGLEPENTILLYVTTAL 161  
 Db 70 LTRRKALGRRAEWLG- -EEAAEADILYLRLGKVERDFEALGVPEAKD-----M 117

Qy 162 FKEAVFMCNVFLHYGLDVHNGDVIRIPLPQVQLEMPDVNRLVPDPFENTH---R 216  
 Db 118 LRAYAGVNAFLAGA---PL PVEYGLGAE---PEPWEPHSLAVMR 159

Qy 217 SIGEFPVYPTPFPYNTGLCHLHDCVIAPIAVLVRVNTAV---ARGAAHIAFDENHEG 272  
 Db 160 RLG-----LLMGSVWPKLWRMLALPVGAANALKURYDDGGRD 197

Qy 273 AV-IPFDITYTYFQSSSSCTTARGARRDNDVNSTSKPSSQGPYFPER---RLAS---IM 322  
 Db 198 LLCPGGAADRLEADLTLRPAVDALLKAMGDASDAGGGNNNWAAPGRBTATGRPL 257

Qy 323 AADTAHALHAYVINTGIVYEETPTDIKEWPKMFIGEKGTLPLRNLALGSSYTTARVAGVGMVFS 382  
 Db 258 AGDPHRVFEI---PSMYAQHHLACDRFDN-IGL---TVP-----GPGFPHFA 298

Qy 383 PNSA-----IYLTEVEDSGTE-----AKDGGGPSPENRP 412  
 Db 299 HNGKVAYCITHAFMDIHDLYLEQPAGEGTTARFGNDFFPVAWSRDRTAVRGGADREDDIV 358

Qy 413 YQFASPHLLANPOTRDGIVLSSGSGNTNTFSDVYLALLCGFAPLARLFLYERCD 472  
 Db 359 ETRHGPVIAQDP---RDGAHTLRSQFETDLSFDCLTRMP---GASTVAGLY---D 407

Qy 473 AGAFTG- -GH---GDAKLYVUTGTGFEDSEIPLCSLCEKHTRPAVCAHTVHLR-----ORMP 521  
 Db 520 DAAATHADLTLSP-----HYGDLRRLREALGARDSSAEEGRMLVANDGRMDAASEVASA 574

Qy 609 HPTPRILDTD---RARIEQTTQ-----FNUKVIVETRDYKIREG--- 645  
 Db 575 YNAPRPLAHTLVLTPSGLEPAISHPAAVARYGVSPOQGVWAWPTLRLDDAGMLKCNWSW 634

Qy 646 ---LSEA-----THSMALTFDPYSGAFCP 666  
 Db 635 DQALSEALSVASQNLTGRIWGEHHRPFTPLATOQFPAWGLLNP 679

Qy 730 YQFAGPHLAAMPQTDDGIVLSSQSTGSNTFSDYALICGFGPILLARLFLYERCD 472  
 Db 799 HNGKVAYCITHAFMDIHDLYLEQPAGEGTTARFGNDFFPVAWSRDRTAVRGGADREDDIV 358

Qy 833 PNSA-----IYLTEVEDSGTE-----AKDGGGPSPENRP 412  
 Db 359 ETRHGPVIAQDP---RDGAHTLRSQFETDLSFDCLTRMP---GASTVAGLY---D 407

Qy 413 YQFAGPHLAAMPQTDDGIVLSSQSTGSNTFSDYALICGFGPILLARLFLYERCD 472  
 Db 473 AGAFTG- -GH---GDAKLYVUTGTGFEDSEIPLCSLCEKHTRPAVCAHTVHLR-----ORMP 521

RESULT 30  
 US-07-935-312-3  
 Application US/07935312  
 Patent No. 5320948



ATTORNEY/AGENT INFORMATION:  
 NAME: Oblon, No. 5336613man F.  
 REFERENCE/DOCKET NUMBER: 24, 618  
 TELECOMMUNICATION INFORMATION:  
 PHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 773 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-019-870-1

Query Match 1.6%; Score 101.5; DB 1; Length 773;  
 Best Local Similarity 21.9%; Pred. No. 1.4; Gaps 19;  
 Matches 91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

US-08-019-870-6

Query Match 1.6%; Score 101.5; DB 1; Length 773;  
 Best Local Similarity 21.9%; Pred. No. 1.4; Mismatches 139; Indels 145; Gaps 19;  
 Matches 91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;

Query Match 1.6%; Score 101.5; DB 1; Length 773;  
 Best Local Similarity 21.9%; Pred. No. 1.4; Mismatches 139; Indels 145; Gaps 19;

US-08-019-870-6

Query 372 VAGVIGAMWFSNSA-----LYLTVEDSGMT-----AK 401  
 Db 287 VPGVGPFFIAFGKVA2XVTHAFMDIHDLYLEQFAGGRTRAFGNDPEPVAWSRDRIV 346

Qy 402 DGGPPSFNSRFYQFAGPHLAANPQTDRDGHVISSOSTGSNTNTFSVDYLALICGFAPLI 461  
 Db 347 RGGADREFDIVETRHPVIAQDP--RDGAATLTLRSQFAETDLSFCLTMP--GASTV 401

Qy 462 ARLLFYLECDAGATG--GH---GDAKLYTGTGFDSEIPCSLCEKHTRPVCAHTTVHR 515  
 Db 402 AQLY-----DATRGWGLIDHNLVAGDVAGSIGHLVRARVSPRENGMLPVPGWSEHE 455

Qy 516 LR-----QRMPIRGQATROPIGYFTGTMNSQY-----SDCDPLGNAYF----- 553  
 Db 456 WRGMIPHEAMPR--VIDEPGGIIVTANRVAADDHPDLCDCHP---PYRABRIMK 507

Qy 554 LILRKPGDQTEAAKATMOTDYLTRALRFLDQERLILRQGA--PCSSEGLSSVIV--- 553  
 Db 508 RLVANPAFAVDDAAAHADLSP-----IVGLLRRLEALGARDSSAASLRQMLVADG 562

Qy 608 -----DHPTRRILDTL--RARIEQTTQ-----FMKVLTET 637  
 Db 563 RMDAASEVASYNAFRALTRLDRGQIAISHPPFAAVAPVSPGQSQWWAVPTLIRD 622

Qy 638 RDYKIREG-----LSEA-----THSMALTDPYGSAFCP 666  
 Db 623 DDAAGMLKGWSWDQALSEALSVASVONLTGRSGWBEHRPRFTHPLATOPPAWAGLNP 678

RESULT 33  
 US-08-019-870-6  
 Sequence 6, Application US/08019870  
 Patent No. 5336613

GENERAL INFORMATION:  
 APPLICANT: NIWA, MINEO  
 APPLICANT: YOSHIMASA, SAITO  
 APPLICANT: SASAKI, HITOSHI  
 APPLICANT: ISHII, YOSHINORI  
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESSSEE: P.C.  
 STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

RESULT 34  
 US-08-019-870-9  
 Sequence 8, Application US/08019870  
 Patent No. 5336613

GENERAL INFORMATION:  
 APPLICANT: NIWA, MINEO  
 APPLICANT: YOSHIMASA, SAITO  
 APPLICANT: SASAKI, HITOSHI  
 APPLICANT: ISHII, YOSHINORI  
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ADDRESSSEE: P.C.  
 STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/019, 870  
 FILING DATE: 19930219  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Oblon, No. 5336613man F.  
 REGISTRATION NUMBER: 24, 618  
 REFERENCE/DOCKET NUMBER: 18-791-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-019-870-8

Query Match 1.6%; Score 101.5; DB 1; Length 774;  
 Best Local Similarity 21.9%; Pred. No. 1.4; Mismatches 41; Indels 145; Gaps 19;  
 Matches 91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;  
 US-08-019-870-11

Query 372 VAGTIGAMYFSPNSA-----LYLTIVEDSGMTB-----AK 401  
 Database 288 VPGPFPFFPAHNGKVAUTHAFMDHILYLFQFAGSRTARFGNDDEPWAWSRDIAY 347  
 Query 402 DGGPSPSFNPYFQAGPHLAANPOTRDGHVLSQSTGSSNTESVYDYLALICFGFAPLL 461  
 Database 348 RGGADREFDVFETHGPVAGDP--RGGAAITLRSVQFATELDSLDTLMP--GASTV 402  
 Query 462 ARLLFYLERCDAAGFTG--GH--GDALKYVGTGTFDSEIPCSLCEKHTRCAHTTYVR 515  
 Database 403 AQLY-----DATRGWGLIDHNLVAGDVAGSIGHLVRARVSPRENGWLPYEGWSGHE 456  
 Query 516 LR----QRMPRFQGATRQFQIGVGTGMSQY-----SDCDPQNYAPY-----  
 Database 457 WRGNTPHEAMPF---VIDPGGIVLVTANNRYYVADDHPDYLCTCHP---PRAERIMK 508  
 Query 554 LILRKPGDQCTEAATAKTMQDYLRTALERLTLDEPBLRLLDRA - PCSSBGLSSVIV---- 607  
 Database 509 RLVANPAFAVDDAARIHAATLSP---HVGLLRRLLEAGARDDSAAEGLRQMLVADG 563  
 Query 608 -----DHPTRPRLDTL---RARIEOTTQ----FMKVILVET 637  
 Database 564 RMDAASEVASAYNAFRLVTRLDRSGLEQASIPFAAVAPGVSPQGOWWAVPTLIRD 623  
 Query 638 RDYKREG----LSEA-----THSMWLTDFPYSGAFCP 666  
 Database 624 DDAGMLKGWWDQASEALYASVASONLTGRWGEERPRTHPLATQFPAWAGLNP 679

RESULT 35  
 US-08-019-870-11  
 Sequence 11, Application US/08019870  
 Patent No. 5336613

GENERAL INFORMATION:  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 APPLICANT: NIIWA, MINEO  
 APPLICANT: YOSHIMASA, SAITO  
 APPLICANT: SAKAI, HITOJI  
 APPLICANT: ISHII, YOSHINORI  
 TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE  
 CITY: Arlington

STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOCS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/019, 870  
 FILING DATE: 19930219  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Oblon, No. 5336613man F.  
 REGISTRATION NUMBER: 24, 618  
 REFERENCE/DOCKET NUMBER: 18-791-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: 248855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-019-870-11

Query Match 1.6%; Score 101.5; DB 1; Length 774;  
 Best Local Similarity 21.9%; Pred. No. 1.4; Mismatches 41; Indels 145; Gaps 19;  
 Matches 91; Conservative 41; Mismatches 139; Indels 145; Gaps 19;  
 US-08-019-870-11

Query 372 VAGTIGAMYFSPNSA-----LYLTIVEDSGMTB-----AK 401  
 Database 288 VPGPFPFFPAHNGKVAUTHAFMDHILYLFQFAGSRTARFGNDDEPWAWSRDIAY 347  
 Query 402 DGGPSPSFNPYFQAGPHLAANPOTRDGHVLSQSTGSSNTESVYDYLALICFGFAPLL 461  
 Database 348 RGGADREFDVFETHGPVAGDP--RGGAAITLRSVQFATELDSLDTLMP--GASTV 402  
 Query 462 ARLLFYLERCDAAGFTG--GH--GDALKYVGTGTFDSEIPCSLCEKHTRCAHTTYVR 515  
 Database 403 AQLY-----DATRGWGLIDHNLVAGDVAGSIGHLVRARVSPRENGWLPYEGWSGHE 456  
 Query 516 LR----QRMPRFQGATRQFQIGVGTGMSQY-----SDCDPQNYAPY-----  
 Database 457 WRGNTPHEAMPF---VIDPGGIVLVTANNRYYVADDHPDYLCTCHP---PRAERIMK 508  
 Query 554 LILRKPGDQCTEAATAKTMQDYLRTALERLTLDEPBLRLLDRA - PCSSBGLSSVIV---- 607  
 Database 509 RLVANPAFAVDDAARIHAATLSP---HVGLLRRLLEAGARDDSAAEGLRQMLVADG 563  
 Query 564 RMDAASEVASAYNAFRLVTRLDRSGLEQASIPFAAVAPGVSPQGOWWAVPTLIRD 623  
 Query 608 -----DHPTRPRLDTL---RARIEOTTQ----FMKVILVET 637  
 Database 624 DDAGMLKGWWDQASEALYASVASONLTGRWGEERPRTHPLATQFPAWAGLNP 679

Search completed: June 3, 2004, 07:15:17  
 Job time : 34 SECS

Result No.	Score	Query Match	Length	DB ID	Description
1	6294	100.0	1203	12	US-09-769-699-2 Sequence 2, Appli
2	3054	48.5	1452	13	US-10-050-673-2 Sequence 2, Appli
3	3015.5	47.9	1196	14	US-10-237-551-00 Sequence 200, App
4	3015.5	47.9	1196	14	US-10-237-551-00 Sequence 232, App
5	3015.5	47.9	1196	14	US-10-237-551-00 Sequence 231, App
6	789	12.5	274	14	US-10-237-551-331 Sequence 230, App
7	736	11.7	248	14	US-10-237-551-330 Sequence 9121, App
8	123.5	2.0	850	14	US-10-156-761-9121 Sequence 34, App
9	123.5	2.0	2597	12	US-10-154-351-34 Sequence 358, App
10	123	2.0	1074	12	US-10-206-576-394 Sequence 394, App
11	123	2.0	1074	12	US-10-206-576-394 Sequence 45763, A
12	121	1.9	2358	12	US-10-282-122A-45763 Sequence 2, Appli
13	120.5	1.9	2597	9	US-09-905-129-2 Sequence 10, Appli
14	120.5	1.9	2597	9	US-09-905-129-13 Sequence 13, Appli
15	120.5	1.9	2597	9	US-09-991-630-2 Sequence 2, Appli
16	120.5	1.9	2597	9	US-09-991-630-10 Sequence 10, Appli
17	120.5	1.9	2597	9	US-09-991-630-13 Sequence 13, Appli
18	120.5	1.9	2597	12	US-10-454-351-2 Sequence 2, Appli
19	120.5	1.9	2597	12	US-10-454-351-10 Sequence 10, Appli
20	120.5	1.9	2597	12	US-10-454-351-13 Sequence 13, Appli
21	120.5	1.9	2597	12	US-09-729-485A-2 Sequence 2, Appli
22	120.5	1.9	2597	12	US-09-729-485A-10 Sequence 10, Appli
23	120.5	1.9	2597	12	US-09-729-485A-13 Sequence 13, Appli
24	120.5	1.9	2597	12	US-09-729-485A-325 Sequence 2, Appli
25	120.5	1.9	2597	12	US-10-211-156A-325 Sequence 10, Appli
26	120.5	1.9	2597	12	US-09-802-318-2 Sequence 13, Appli
27	120.5	1.9	2597	12	US-09-902-318-13 Sequence 11, Appli
28	1120	1.9	5245	14	US-10-329-079-11 Sequence 7150, A
29	1118	1.9	452	12	US-10-425-114-71520 Sequence 1957, Ap
30	1118	1.9	19608	15	US-10-084-846A-8 Sequence 8, Appli
31	114.5	1.8	1479	12	US-10-211-156A-325 Sequence 87, Appli
32	114.5	1.8	1496	12	US-10-211-1462-87 Sequence 125, Appli
33	114.5	1.8	1496	14	US-10-021-660-125 Sequence 125, Appli
34	114.5	1.8	1496	14	US-10-331-496A-28 Sequence 28, Appli
35	114.5	1.8	1498	12	US-10-276-774-397 Sequence 1957, Ap
36	114.5	1.8	1498	12	US-10-243-552-899 Sequence 899, Appli
37	113.5	1.8	1477	14	US-10-274-583-20 Sequence 20, Appli
38	113	1.8	1682	12	US-10-282-122A-64702 Sequence 64702, A
39	113	1.8	1787	12	US-10-282-122A-62625 Sequence 62625, A
40	113	1.8	2505	12	US-10-205-331-20 Sequence 20, Appli
41	112	1.8	943	12	US-10-282-112A-68197 Sequence 68197, A
42	112	1.8	3868	16	US-10-461-194-103 Sequence 290, Appli
43	112	1.8	6620	16	US-10-080-334-590 Sequence 291, Ap
44	112	1.8	6620	16	US-10-408-765A-2291 Sequence 67862, A
45	111.5	1.8	4317	12	US-10-282-122A-77862 Sequence 2, Appli
46	111	1.8	5215	9	US-09-861-219-2 Sequence 2, Appli
47	111	1.8	5215	9	US-09-860-846-2 Sequence 2, Appli
48	111	1.8	5215	10	US-09-988-384B-2 Sequence 2, Appli
49	111	1.8	5215	10	US-09-836-621-2 Sequence 45, Appli
50	111	1.8	5215	14	US-10-271-889-45 Sequence 246, Appli
51	10.5	1.8	3069	14	US-09-712-363-246 Sequence 934, Appli
52	110	1.7	771	16	US-10-389-156-934 Sequence 68623, A
53	110	1.7	784	12	US-10-282-122A-68623 Sequence 7942, A
54	110	1.7	1039	12	US-10-282-112A-77942 Sequence 2, Appli
55	109.5	1.7	2630	13	US-10-077-130-2 Sequence 5, Appli
56	109.5	1.7	7968	13	US-10-077-130-5 Sequence 372, Appli
57	109	1.7	2845	12	US-10-267-50-372 Sequence 250597, App
58	108	1.7	386	12	US-10-424-519-250597 Sequence 250597, A
59	108	1.7	499	12	US-10-369-493-10577 Sequence 10577, A
60	108	1.7	499	14	US-10-369-493-10577 Sequence 6, Appli
61	107.5	1.7	8026	14	US-10-132-134-12 Sequence 12, Appli
62	107	1.7	905	15	US-10-369-493-2505 Sequence 2550, Ap
63	107	1.7	1279	12	US-10-332-288-5 Sequence 6, Appli
64	106.5	1.7	1299	14	US-10-156-761-12449 Sequence 12449, A
65	106.5	1.7	2448	12	US-10-210-172-48 Sequence 48, Appli
66	106.5	1.7	3298	12	US-10-334-143-34 Sequence 50, Appli
67	106.5	1.7	3298	14	US-10-160-158-16 Sequence 16, Appli
68	106.5	1.7	3298	14	US-10-174-677-8 Sequence 8, Appli
69	106.5	1.7	3298	15	US-10-120-301-51 Sequence 51, Appli
70	105.5	1.7	707	14	US-10-156-761-9979 Sequence 9979, Ap
71	105.5	1.7	1052	16	US-10-389-516-608 Sequence 608, App
72	105.5	1.7	1053	15	US-10-334-143-34 Sequence 34, Appli
73	105.5	1.7	1967	14	US-10-219-814-85 Sequence 575, Appli
74	104.5	1.7	1967	14	US-09-051-847-55 Sequence 1, Appli
75	104.5	1.7	635	16	US-10-225-56A-755 Sequence 575, Appli
76	104.5	1.7	635	16	US-10-043-233-5 Sequence 1, Appli
77	104.5	1.7	1471	8	US-08-811-519A-1 Sequence 8, Appli
78	104.5	1.7	1515	14	US-10-340-154-8 Sequence 1101, Ap
79	104.5	1.7	2530	12	US-10-396-115-1101 Sequence 16, Appli
80	104.5	1.7	6304	14	US-10-147-0-16-16 Sequence 10, Appli
81	104	1.7	3192	14	US-10-332-134-10 Sequence 65528, A
82	103.5	1.6	495	12	US-10-325-114-65528 Sequence 57721, A
83	103.5	1.6	942	12	US-10-382-122A-5721 Sequence 920, App
84	103.5	1.6	1750	12	US-10-043-555-920 Sequence 7819, A
85	103	1.6	1050	12	US-10-382-122A-78119 Sequence 4, Appli
86	103	1.6	3472	13	US-10-027-806-4 Sequence 4, Appli
87	103	1.6	3472	14	US-10-027-801-4 Sequence 4, Appli
88	103	1.6	3472	14	US-10-027-801-4 Sequence 4, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6294	100.0	1203	12	US-09-769-699-2 Sequence 2, Appli
2	3054	48.5	1452	13	US-10-050-673-2 Sequence 2, Appli
3	3015.5	47.9	1196	14	US-10-237-551-00 Sequence 200, App
4	3015.5	47.9	1196	14	US-10-237-551-00 Sequence 232, App
5	789	12.5	274	14	US-10-237-551-331 Sequence 231, App
6	736	11.7	248	14	US-10-237-551-330 Sequence 230, App
7	123.5	2.0	850	14	US-10-156-761-9121 Sequence 9121, App
8	123.5	2.0	2597	12	US-10-154-351-34 Sequence 34, App
9	123.5	2.0	1074	12	US-10-206-576-394 Sequence 358, App
10	123	2.0	1074	12	US-10-206-576-394 Sequence 394, App
11	121	1.9	2358	12	US-10-282-122A-45763 Sequence 45763, A
12	120.5	1.9	2597	9	US-09-905-129-2 Sequence 2, Appli
13	120.5	1.9	2597	9	US-09-905-129-10 Sequence 10, Appli
14	120.5	1.9	2597	9	US-09-905-129-13 Sequence 13, Appli

ALIGNMENTS											
SEQUENCE 1											
89	103	1.6	3472	14	US-10-029-120-4	Sequence 4, AppD1	Qy				
90	102	1.6	625	12	US-10-282-122A-47996	Sequence 47996, A	Db				
91	102	1.6	876	12	US-10-282-122A-62122	Sequence 62122, A					
92	102	1.6	1074	15	US-10-369-493-359	Sequence 359, App					
93	102	1.6	4590	11	US-10-970-944-21	Sequence 21, App1					
94	102	1.6	4590	14	US-10-160-758-13	Sequence 13, App1	Qy				
95	102	1.6	4590	14	US-10-160-758-14	Sequence 14, App1	Db				
96	102	1.6	4590	14	US-10-060-036-157	Sequence 157, App					
97	102	1.6	4590	15	US-10-295-027-1323	Sequence 1323, AP					
98	101.5	1.6	1028	14	US-10-124-714-8088	Sequence 8088, AP	Qy				
99	101	1.6	336	12	US-10-425-114-70947	Sequence 70947, A	Db				
100	101	1.6	587	12	US-10-282-122A-50633	Sequence 50633, A					
SEQUENCE 2											
Sequence 2, Application US/09761699											
Publication No. US2001003901A1											
GENERAL INFORMATION:											
APPLICANT: Silverstein, Saul J											
APPLICANT: Lungu, Octavian											
APPLICANT: Gershon, Anne A											
APPLICANT: Annunziato, Paula W											
TITLE OF INVENTION: VZV ORF29p Protein-Related Compositions and Methods											
CURRENT APPLICATION NUMBER: US/09/769, 699											
CURRENT FILING DATE: 2002-04-22											
NUMBER OF SEQ ID NOS: 2											
SOFTWARE: Patentin version 3.1											
SEQ ID NO 2											
LENGTH: 1203											
TYPE: PRT											
ORGANISM: Varicella zoster											
S-09-769-699-2											
Query Match Score: 6294; DB 12; Length: 1203;											
Best Local Similarity: 100.0%; Pred. No. 0;											
Matches 1203; Conservative: 0; Mismatches: 0; Indels: 0;											
1 MENTQKTVTVPGLGVYAAVVEDDLETSPLALARSTDSDALLPLMNLTVBKTFTS 60											
1 MENTQKTVTVPGLGVYAAVVEDDLETSPLALARSTDSDALLPLMNLTVBKTFTS 60											
1 SLAVVSGARTGTLGAGCTLKLTTSHFYPVFGGKHLVPLSSAAPNLTRACNARERF 120											
61 SLAVVSGARTGTLGAGCTLKLTTSHFYPVFGGKHLVPLSSAAPNLTRACNARERF 120											
61 SLAVVSGARTGTLGAGCTLKLTTSHFYPVFGGKHLVPLSSAAPNLTRACNARERF 120											
121 GFSRCQGPPVDAVETGAEICTRGLBPENTILYLVTLFKEAVFMCMVFLHYGLDI 180											
121 GFSRCQGPPVDAVETGAEICTRGLBPENTILYLVTLFKEAVFMCMVFLHYGLDI 180											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGEFGVYPPFPYNTGLCHLJHDC 240											
181 VHNHEDVTRIPFLPIOLMPDNRLYDPEMTNTHRSIGE											

;

TYPE: PRT

ORGANISM: herpesvirus

US-10-050-673-2

Query Match 48.5%; Score 3054; DB 13; Length 1452;

Best Local Similarity 49.8%; Pred. No. 5e-294;

Matches 609; Conservative 200; Mismatches 366; Indels 48; Gaps 17;

Qy 1 MENTOKTVT---VPRGPIGVY--ACRVEDDLEISFLAARSSTDSDLALPLMRNLTE 55

Db 1 METKSKTATIKVPPPEPLGVYARACPSEGIEL--LALLSARSQSDADYAVPLVYGLTE 58

Qy 56 KTFITSLAVVSLAVSAGARTTGLAGAGITGTTTGYPRVFGREVLPSAANPNTTNA 115

Db 59 SGFEANAVVAVVUGSRTGTLGGTAVSLLKUTPHEYSSVYVFGGRHLDPSQAPNTRLCE 118

Qy 116 ARERFGFSRCQGPPVGDGAVETTGAELCTRIGLEPENTILYLVTAFLKEAVFMCNVFLHY 175

Db 119 ARRHF0FSDTTPRGILKHETGEALCERGLDPRALLLVLVTEGFKEAVCINNTFLIL 178

Qy 176 GGLDITHINHGCVIRPLFVQLEMFVNLVPDPFNTHRISIGEGFVYPTPFYNTGLCH 235

Db 179 GGSDKTGTGAAVALAEVHRPVYPLQLENMDPSVIAEPPNANRISIGNFTYPLPFNRPINR 238

236 LHIDCVIAPIAVAHLYRNTAVGAAHLFEDNEHGAFLPDTITYFQSSSSGTTAR 295

Qy 239 LLFEATVGPAAVALCRNVAVARAAHLFEDNEHGAFLAPADITFTAFAEASOG - KTPR 296

Db 296 GARRNDVNSTSKPSPGGFEBRLLASTMAAIDLHAEVNTGIEETPTDIKEKMPMF1GM 355

Qy 297 GGR ---DG3GKGPGGPFERPLASMGAAHALESTISMAVPEDEPPDUSAPLCEQ 351

Db 356 EGTLPLRNALGSYTAVARVIGAMYFSPNALSALYTEVEDSGMTEAKDGGGPSNRFYOF 415

Qy 352 DTAARANAVGAYLARAAGLNGAMYFSTNSALHLTEVDGGPAPDKDHSK-PSYRFFLY 410

Qy 416 AGPHLLANQCDRDGHVU-----SSQSTGSSNTTEFSVUDYLALICGFGRPLAARLLFY 468

Db 411 PGTIVANPQYDREGHIVPGFEGRPPAPLNGTQ -EFAIGHLAMLGCFSSLALLKMLPFL 469

469 ERCDAGAFTGGHG -DALKVITGTFDSEBIPSCLCEKTRPYCAGHTVHLRQMRPFGQAT 527

Qy 470 ERCDGGYIVGROEMDVERVADSDNQDVPNCNLCTPDRACVHTTLMRARHFKPASA 529

Db 528 RQPIGYGTMSQYSDDPDLYNAYPLILRKFGDQTEAAKATMDQTYRATLERFIDLQ 587

Db 530 RGAIGVGTMSYMSCDVILGNYAASALRK-ADGSETARTIMQETYRATERWMAELT 589

Qy 588 ERLLDRCAPSSSEGGLSSVIVDHPPTERRLDTLRARLEOTTIQFMKVLYTERDYKIREGUS 647

Db 589 LQYDQAVPTANGRLETITRREALHTVVMVQDVREQMLNLYSERNFKERDGLG 648

Db 648 BATHSMALTFDPSGAFCPITNLFLVERTHLAVYDQLASOCHCFYGOOQEGRNFRNQFO 707

Db 649 EAHANHSILTDYIAGCPCQQLLGRNSNLAQYDIALSQCQGVZAGSQVEGRNFRNQFO 708

Qy 708 PYLRRFVLDENGFF1STRSITVTLSEG -PVSAPNPTLGQDODAAGRTFEDSLARVSYEVI 766

Db 709 PYLRRYMDMENGLNGELSAKLTIVALESEGAAICAPSLTAGQTAPEASSFEDVARTLGFPP 768

Qy 767 RDLRVRDVRVVFEGNCNTNLSEARAPARLVGLAYQROEKRDMLHAGLGFLKOFGLLFP 826

Db 769 KEIWKSRVLFENGASANASEAKARYASLQSAVOKDKRVDILGFLGFLLKOFGLAIFP 828

Qy 827 RGMPPNSKSPNQFWTFLLORNQMPAKLTHEITIAAVRTERYAAINFNLNPTCI 886

Db 829 NGKPPGQNQNPQFWTFLQWTAQNOLPARLSSREDIETIAFKKPSLDYGAINFNLNAPNN 888

Qy 887 GELAQFTMANLTLKYCDHSQYINTLTSITGARRPRDPSVYLHTRKDTSAAADIEQAA 946

Db 889 SELAMYNNANQILRYCDHSYINTLTAIAGSRRPPSVQAAAW --SAQGGGLEA7Q 945

Qy 947 KALLEKTENLPELWHTAFTSTHLVRAAMQRFMVYGLISISKYHGAAGNTRVFOAGNNSG 1006

Db 946 RALMDATDAHPGAWNTMSMASCNLRLREMAAARPMVYTLGLSISKYNGANDVFQAGNWAS 1005

Qy 1007 LNGGKNCPPLFDFDRTRFLACPRGGFICPVTGPSSGNRETTLSPOVGRIVSGGAMVQ 1066

Db 1006 LNGGKNCPPLFDFTRKFLACPRGFVCAASNLUGGAHESSLCLCQLGTTSEGAAVA 1065

Qy 1067 LAIATVTVRAVGARAQMAFDWLSTTDEFTLARDLQELHQIQTLETPTVEGAL--- 1123

Db 1066 SSYFVATVKSLSPLRTQQLQIEWLALLEDVLESEEMELTARALERGNGESTDAALEVA 1125

Qy 1124 -PAVKILDEKTTAGDGETPTNLIAENFD - -SCBSPSHDTTSVNLNTISGNSNISTVEGKRP 1180

Db 1126 HEA8ALSQLGNRAGE-----VNFRDFGCE-----DDNATPFGGDPGAPGAPGRKRA 1173

Qy 1181 PEDDEFLDSLGIPIKHNIGNTM 1203

Db 1174 FHDDDPFG-EGPPDKKQDLDLDM 1195

RESULT 3

US-10-200-562-200

Sequence 200, Application US/10200562

Publication No. US20030165819A1

GENERAL INFORMATION:

APPLICANT: McCown, Patrick

APPLICANT: Hosken, Nancy A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

FILE REFERENCE: 210121.538C2

CURRENT APPLICATION NUMBER: US/10/200-562

CURRENT FILING DATE: 2002-07-19

NUMBER OF SEQ ID NOS: 212

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 200

LENGTH: 1.196

TYPE: PRT

ORGANISM: HSV2

US-10-200-562-200

Query Match 47.9%; Score 3015.5; DB 14; Length 1196;

Best Local Similarity 49.0%; Pred. No. 2.5e-200;

Matches 595; Conservative 213; Mismatches 366; Indels 41; Gaps 16;

Qy 4 TOKTVYPTGPIGYVY - -ACRVEDDLEEEISFLAARSTDSDLALLPLMRNLTYEKPTTSS 61

Db 7 TTITVKVPPGPMGYVYGRACPARGLEE - -LSSLISARGSDADAVPLVGLTVEGGBAN 64

62 LAVSGAIRTGTTGLGAGITKLTSHPSVPSVYFHGGHVLPSSAAAPNLTRACNAARRFG 121

Db 65 VAATVGSRTGLGUGTAVSLKLMPSHYSPSVYFHGGHVLPSSAAAPNLTRACNAARRFG 124

Qy 122 FSRQGQPPVDPGAVETTGAETCRGLPEENTLYLVTAFLKEAVNCVNFLYHGGDIV 181

Db 125 FADYAPRCPDLCRHTTGDALCERLGLDPRALLYLVTEGFREAVCISNTFLHGGDKV 184

Qy 182 HINHGDIVIRIPLFPVQLPMDVRLVPPDFNTHRS - GEGFVYPTPYNTGLCHLIDCV 241

Db 185 TIGDAEVIRIPVPLQMTDFPRLVDFPNCNHRSGENFNYPLPFPNRPLARLIEAV 244

Qy 242 IAPMVAFLRVNTAVAGAAHAFDENHEGAVLPPDITYTQOSSSGTTARGAREN 301

Db 245 VGPAAVAKARNAVAAHAFDENHEGAVLPPDITYTQOSSSGTTARGAREN 301

Qy 302 VNSTSKPSGGFERRLASMADDTALHAEVINTGIEYBTPDIKEWPMFICMEGTILPR 361

Db 300 - -DAGNKGPGAGGFQRLASVMAVDEPPDDITWPLBEGQETPAA 357

362 LNALGSYTAVARVAGYIGAMFSPSIALYLTEVEDSGMTEAKDGPGPSPNRFYQFAGPHLA 421

Db 358 AGAVGAYLARAAGLIVGVNDFSTNSALHTEVDAGAPPKDHSK-PSYRFFLVPGTHVA 416

Qy 422 ANPQTDRDGHVU-----SSQSTGSNTSFVSYDYLALICGFQAPLLFLYLERCDAG 474



RESULT 5  
US-10-237-551-232  
; Sequence 232, Application US/10237551  
; Publication No US20030165820A1  
; GENERAL INFORMATION:  
; APPLICANT: Day, Craig H.  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Parsons, Joseph M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF HERPES SIMPLEX VIRUS INFECTION  
; FILE REFERENCE: 210121.538C3  
; CURRENT APPLICATION NUMBER: US/10/237,551  
; CURRENT FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSEQ For Windows Version 4.0  
; SEQ ID NO: 232  
; LENGTH: 1196  
; TYPE: PRT  
; ORGANISM: Herpes simplex virus

US-10-237-551-232

Query Match 47.9%; Score 3015.5; DB 14; Length 1196;  
Best Local Similarity 49.0%; Pred. No. 2.5e-290;  
Matches 595; Conservative 213; Mismatches 366; Indels 41; Gaps 16;

Qy 4 TOKVTVTPRGPLGVY-  
Db 7 TTTVKVPPGPMGVYGRACBQEL-  
Qy 62 LAVSGARTGLAGAGITKLTKTSHFYPSTVPHGGKHLVPSAAAPNLTRACNAARERFG  
Db 65 VAAVGSRTTGLGSTAVSLKMLPSHSSVYVPHGRHLAPSTQAPNLTRICERARPHFG  
Qy 122 FSRQGPPYDGAVTTGABCTPBLGLEPENTLYLYTPTALKEAVENCNVPHYGGSDIV  
Db 125 FADYAPRCPDLKHEETGDALECRGLDDRLALYLVTEGFFAEVCAISNTPLHLGNDKV  
Qy 182 HINHGDVRIPLPVQLMFDPNRLVPPDFTNTHRSIPEGFVTPYNTGLCHLIEHDCV  
Db 185 TIGDAEVTRIPVYPLQMFDPESRVIADPFCNHRSGENENYPLPFENRPLARJLFEAV  
Qy 242 TAPKAVALEVRVNTAVARAAHILAFDENTHEAVIINTGIVETPTDIKEWMFIGMEGLP  
Db 245 VGPAAVALARVNDAVARAAHILAFDENTHEGAALPADIITPAEASQG-  
Qy 302 VNSTSKPSKPSGGFERRLASMADTAHAEVINTGIVETPTDIKEWMFIGMEGLP  
Db 300 -DAGNKGPGGFFQRLASVMAAALSISVMAVDEPPDITWPLLEGQETPAAR  
Qy 362 LNALGSYTAVAGVIGAMYPSNSPNSALYLTVEVEDSGMTEAKDGGPSPSFNRYQFAGPHLA  
Db 358 AGAVGAYLARAAAGLVGAMYFSTNSALHTEVDAGDAPDKHSK-PSFYRFLVPGTHVA

Qy 422 ANPQTDRGDHVL-----SSQSTGSSNTESFVDYLALICGFAPILLARLFLYLERCDAG 474  
Db 417 ANPQDREBGFVPGPGRPAFLPGTQ-  
Qy 475 AFTGCHG-DALKYUTGTSEBIPSLCEKTRPICAHTVHRLFORMPRFGQATQPGIV 533  
Db 476 VIVGROEMDVERYADSGQDVPNCNLCTPSTRHACHTTMRARHPKAASARGAIV 535  
Qy 534 FGTGNSQYSDCDPLGNYAPYLIRKPGDQEAAKATMDQTYRATERLFLDQEERLDR 593  
Db 536 FGTGNSQYASDODVLYGNYAASFALSLR-ADGSENTRTMOETYRATAERVMAELEALQYDQ 594  
Qy 594 GAPCSEGSSLSSVIVDHPFPRILDTLRARLEQTITQFMKVLYPRDYKREGLSBATHSM 653  
Db 595 AVPTAIGRLTIGIGRLEHTVNNNIKLVDRVEYOLMENLIEGRNFKRDGLAEEAHM 654  
Qy 654 ALTFDPYSGAFCPTINFLYERTHIAVQDIALSOSCHCVYQOQEVRNQFQEVLRAR 713  
Db 655 SLSLDPTYCGPCPLQLLARSNLAVYQDIALSQCQHVGAGQSVEGRNRFQFQPVLRRR 714  
Qy 714 FVDLFNGGFISTRSTVTLSEG-PVSAAPNPLGODAPGRTFDGDLARYSVEVIRDIVK 772  
Db 715 VMDLFNGFISAKTIVLSEGAACPSLTAQGTAPESSFEGDVARVTLGFPKELRVK 774  
Qy 773 NRUVPSGNCNPNLSEARARLVGLASAYQREKRDMLHAGLGEKLFQFGMPPN 832  
Db 775 SRVLPGAGSANASEAKARYASLQAYKDPKRYDILGFLGFLKQFHAFVPGKPPG 834  
Qy 833 SKSPNQFWTLLQNQMPDLTHEEITIAVYKRFTEYYAAMFNLPTCIGELAQF 892  
Db 835 SNQPNPQFWTALQRNOLPARLSSDEDIETIAFKRFSUDYGAINFOINLAPNNTSELAMY 894  
Qy 893 YMANLILKYCDHSQYLINTNTSITGARRRDPDSSVHLWIKDVTSAIDETQAKALEK 952  
Db 895 YMANQOLRYCDHSTYFINTLTAVIAGSRPPSPVQAAAMAPQ--GGAGLEAGARALMD 951  
Qy 953 TENLPPLWTAFTSTLVRAMNOEPMVYIISISKYHGAGNNRVRQGNGNSGNGN 1012  
Db 952 LDAHPAWTSMEASCNLRLPVMARPMWVGLSKYGMAGNDRVFQAGNWALJLGGN 1011  
Qy 1013 VCPLETFDTRPREFITACPRGGFICPVTGPGSGNRETTLSQVQRGTTIVSGAMVOLAYAT 1072  
Db 1012 ACPLTFDTRPKVFIACPRGFVCAISLGGAEHSLCQLRE-TAEGGAAVASSVFA 1071  
Qy 1073 VRAYVGRAGQHMAFDWLSLTDEPLARDLEELHDQIQTLETPTWVEGAL---EAVKI 1128  
Db 1072 TVKSLGPRTQOLQEDWLAILEDTSSEEMEFTTRALERGHGEWSTDALVEAHEREAL 1131  
Qy 1129 LDEKITAQDGETPTNLAENDSCEPSHDTTSNMINISGNTGTVPGKRPDPDELF 1188  
Db 1132 VSQLGAGE---VNTGDFGDEDIDHAASPEGGLAA--AGRAVGARKRAFHGDDPFG 1182  
Qy 1189 LSGIPIKHGNITMEM 1203  
Db 1183 -EGPPEKK-DITLDW 1195

RESULT 6  
US-10-237-551-231  
; Sequence 231, Application US/10237551  
; GENERAL INFORMATION:  
; Publication No. US20030165820A1  
; APPLICANT: Day, Craig H.  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Parsons, Joseph M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF HERPES SIMPLEX VIRUS INFECTION  
; FILE REFERENCE: 210121.538C3  
; CURRENT APPLICATION NUMBER: US/10/237,551  
; CURRENT FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 231

LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Herpes simplex virus  
US-10-237-551-231

Query Match 7  
Best Local Similarity 12.5%; Score 788; DB 14; Length 274;  
Matches 153; Conservative 41; Mismatches 75; Indels 2; Gaps 1;  
Qy 28 LEISFIAARSTDSDLALLPLMRNLTVEKTTSSLAIVSGARTTGLAGAGITLKLITTSF 87  
Db 2 LEILSLDARSQDADVAPLVLGTVTESGEFANVAVSVSRTTGLGTTAVS1KMPH7 61  
Qy 98 YPSVEVTHGCKRVLPSAAPNITBACNAAREPFGESBCQGPPYDGAETTSAGCTTGL 147  
Db 62 SPSVYVPHGRHLAPSTQAPNTRCLCRAHRRFGFSYAPRCDLKHETSDALCERLGL 121  
Qy 148 EPNTILYLVTALFKRVEAVMENVPHYGLDIVVHNGDVKTRIPFQVLFMPDVNLV 207  
Db 122 DPPRLYLVLTIGERAVCIENTLFLGMDKVTGDAEVTRIPYPLQMFMPESRVI 181  
Qy 208 PDPFNTHRSIGDFVYPTPFNTGLCHLHHCVIAPMVALVRNNTAVARGAAHLLAFD 267  
Db 1824 ADPNCNHSRISGENFNTPLPFTRPLRLFLFIAVGPBAVALRARNYDVARAAHLLAFD 241  
Qy 268 ENHEGAVLPDPDITTYFOSSSGTTARGAR 298  
Db 242 ENHEGAALPDADITTAFAEASQG -KPGQGAR 270

RESULT 8  
US-10-156-761-9121  
; Sequence 9121, Application US/10156761  
; GENERAL INFORMATION:  
; Publication No. US20030119018A1  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HOBIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADATOSHI  
; APPLICANT: SAKAKI, YOSHITAKI  
; APPLICANT: HATTORI, MASAHIRO  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156, 761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO: 9121  
; LENGTH: 850  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis

Query Match 2.0%; Score 123.5; DB 14; Length 850;  
Best Local Similarity 20.5%; Pred. No. 0.046;  
Matches 182; Conservative 104; Mismatches 327; Indels 273; Gaps 37;

Qy 305 TSKPSPGGFE-----RLASIMAAADTALHAEVFNTGIVYEETPDIKEWPMFIGM 355  
Db 3 TSRRTPSAGLEPPSRPSPYRGRRAFQGPAD-----DGTGDTETTAASADSPVGAGR 54

Qy 356 EGTPR-----INALGUTTARYAVGIVGAMVFPDNAAKILTEVEDSGNTTE 399  
Db 55 WGVRRTPTVRAKIVCLMMPVVSLLAWAY-----ATVSPAQDVARLROYQVQDRTV 105

Qy 400 AKDGGSPGPSPSNRFYQFAGPHLAAMPQTDGDGHVLSQSTGSSNTTEFSDYIAL---TCG 455  
Db 106 RAPVAAVALQARAAAVRHVDDPAAED---SGFTLAAAPDRAVDKLRGGHTYVA 161

Qy 456 EGAPLARLFLYLERCDAGAFTGCHGDAKYVTCFTDFSEIPCSLCEKHTRPVCAHTYHR 515  
Db 162 DGADEAQVGRLETFVSGA-----BQRLSLRG-----AVLER 194

Qy 516 IQRQMRERGATRQDPIGVGSTMN -SQYSDCDP1GNYAAYPLRKPGDOTEAAKATM0D 573  
Db 195 RARMDTEFGYTRTAARFGGALTGIODAD-LGSDARVLL---EFSRAGPALAQED 248

Qy 574 YRATLRLFIDLEQPERL-LDRGAPCSEGSL-SVIVDHPFTERRLDTFARIEQTTCQFM 631  
Db 249 AVLSSRLAQTLDGRLRIFTGAVDTRRLTDTSVAD-----LSEREAAWQGVATGRA 302

Qy 670 FLYKRTHLAVQDIALSOCHCVF----YQQQVEGRNFRNQFQPVLRREFD---LIFNG 720

Db 3 PLVGLTVSGFEANVAAVGSRTGGLGTTAVS1KMPH7 62

Qy 47 PMLNLTVEKTFSTSSLAIVSGARTTGLAGAGITLKLITTSFESVVFHGGKRVLPSSAA 106  
Db 107 PNLTRACNAARERFGFSRCGPPYDGAETTGAEICTRGLPELENTLYVTTALFKEAV 166  
Db 63 PNLTRLCERARRHGFSDYAPRCDLKHETTDALCERLGLDRLYLVTEGFFREAV 122  
Qy 167 FMCNVPLHNGGLDVTNGDVRIPFQVLPMDVNLVPDFTNTHRSCEGFYPT 226  
Db 123 CISNTFLHGGMDKVTGDAEVTRIPYPLQMMMPDSRVIAFPNCNHSRISGENFNYPL 182

Qy 227 PFTNTGLCHLHIDCIVTAPMAVALVRNNTAVARGAAHAFDNEGAVLPDPDITYTVFQS 286  
Db 183 PFPNRPLAKLFLFEAVGPAAVALRARNYDVARAAHAFDENHEGALPADEITFATEA 242  
Qy 287 S 287

Db 462 -----RAELASGISCV----- 472

5 02 DSSPHILEWLLADGSKTYRATPY/SEDGRLLIDNGKLELOMADS/DAHLHCISTNDADADV 561  
 6 40 - -YKIR- -EGLSEATHMALTDPYSGAF---CPTINFLVKRTHLAVYQDLSQSQCHCV 691  
 5 62 LTYRITYVEPYESTHSGVQHTVVTGTCGETDLPCLSIG-----VFDASIS--WI 608  
 6 92 FYGOQYEVGRNPANQFQPYLRRFVDLNGGF1STRSITVLSERPVS--APNPT---- 743  
 6 09 LFGNTVFSQSPDR-----QIUNNGTURILQVTP-KDQGHYQCYAANPSSADFSS 657  
 7 44 -----LGQDAPAGRFTDGLARVSVEVIRDIRVQNRVVFSGNCNTNLSEARAR 791  
 6 58 FKVSVQKGQYRVEHDFEAGGSGLGE PNSSVLSLKOPASLK---LSASALTGSQAKQ- 711  
 7 92 LVGLASYQROERVDMHAGL-FLLQKPHGLPFRGMPPNSKSPNPONFWTILQ--R 847  
 7 12 --VSGYHRKNGKHDLTHRRGDSITLRRFRE -HRROQPLSARRIDPQRWAALIEKAKK 765  
 8 48 NOMPADCLTUEETT-----IAAVRKFTEETAAINFLNLPPTCTIGELAQFYMANLILK 900  
 7 66 NSVP---KKQENTTIVKPVPLVLTDEEKDAGMI-PP----- 802  
 9 01 YCDHSQYQVINTLTSITGARRPRDPSSVHWRKDVTSAADIEQAKALLEKTNELPELW 960  
 8 03 --DEFEMVYLTKASGVGRSPATADSGPYRHGMFTSIASSTEVSIVNPQTLQ-SEHPPDFX 859  
 9 61 TRAFTSHLVRAM-----XQEPMVYVIGISISKYHGAGGNNRVEQAGNMSG-- 1006  
 8 60 LFSVTINGTAVTKSMNPSIASKIEDTNTQNPIIIFFP-SVAEIDRSA-----QAGRASSQS 912  
 1007 --LNGGRNVCPLFTFDITRFLIACPREGFT-----CPVIG---PSGN 1045  
 9 13 AHPPVIGEN---MATYGHNTYSSFTSKASTVLQPINPTESYGPQIPITGVSRPSSSD 966

0 6-576-358  
 1 Application US/10206576  
 2 Application No. US20030017495A1  
 3 TRADE INFORMATION:  
 4 APPLICANT: Choi et al.  
 5 TITLE OR INVENTION: Enterococcus faecalis Polynucleotides and Polypept  
 6 NUMBER OF SEQUENCES: 497  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Human Genome Sciences, Inc.  
 9 STREET: 9410 Key West Avenue  
 10 CITY: Rockville  
 11 STATE: Maryland  
 12 COUNTRY: USA  
 13 ZIP: 20850  
 14 COMPUTER READABLE FORM:  
 15 MEDIUM TYPE: CD-R  
 16 COMPUTER: Dell Latitude  
 17 OPERATING SYSTEM: Windows 98  
 18 SOFTWARE: ASCII Text  
 19 CURRENT APPLICATION DATA:  
 20 APPLICATION NUMBER: US/10/206,576  
 21 FILING DATE: 29-Jul-2002  
 22 CLASSIFICATION: <Unknown>  
 23 PRIOR APPLICATION DATA:  
 24 APPLICATION NUMBER: US 09/071,035  
 25 FILING DATE: 1998-05-04  
 26 APPLICATION NUMBER: US 60/046,655  
 27 FILING DATE: 1997-05-16  
 28 APPLICATION NUMBER: US 60/044,031  
 29 FILING DATE: 1997-05-06  
 30 APPLICATION NUMBER: US 60/066,009  
 31 FILING DATE: 1997-11-14  
 32 ATTORNEY/AGENT INFORMATION:  
 33 NAME: Hyman, Mark J.  
 34 REGISTRATION NUMBER: 46,789  
 35 REDEMPTION/DOCKET NUMBER: PB369P1D1  
 36 DERMINATION FOR SEQ ID NO: 358:

SEQUENCE CHARACTERISTICS:	Qy	993 AGNNRVPQAGNWGLNGGKVNGLNGKVNGLPLFTDRTRFTIACPRGGFCICPTGPSSGNRETTLSD 1052
LENGTH: 1074 amino acids	Db	854 YENKVAEAGNE-----PVA-----
TYPE: amino acid		-----KDAISLNN 875
STRANDEDNESS: single		
TOPOLOGY: linear		
MOLECULE TYPE: protein		
SEQUENCE DESCRIPTION: SEQ ID NO: 358:		
US-10-206-57-358		
Query Match 2.0%; Score 123; DB 12; Length 1074;	Qy	1053 QVRGIVSGAMVQIAATVTVRANGER-----AQMAFDWLSLTDDEFELARDL- 1102
Best Local Similarity 18.3%; Pred. No. 0.078;	Db	876 QAQ-----TWNCTIERHVSQTQKAHLEDGSQTFTSDVMDMFDDSVTHVLD 923
Matches 206; Conservative 150; Mismatches 415; Indels 352; Gaps 52;	Qy	1103 -BEELHDQIQTQLETPWYEGALBAVKTIDE-----KTTAGD-----GETPTNLAFFKEF- 1149
Qy 250 RVRNNTAVARGAAHLADEFENHEGAVLPPDITYFQSSSGFTTARGARRNDVNSTSKPS 309	Db	924 GSKEAEFTTLYALIDGDTKNEIWKGKLEHEVNDKEFVTKLAEKDVKYPESTKEF- 982
Db 67 RTISLYAETNGAKOTVFC-IEPSVSIPTVTHAY-----QKNPL 104	Qy	1150 SCEPSHDTISNV-----LNISGSNISGSSTVPGLKRPEDDE 1185
Qy 310 PSGCFERRASIM--AADPVALHEVIFTGIVEE-----TPTDIKEWPMF 1 353	Db	983 -TEINYEKOGNVNGKHINEDLKEKSQTLTPEKVPTRIPSTPKOPE 1024
Db 105 PMSDKAKCIVSVLWEKAGTDIDTMVMAQKMINVEVNGYKLHSIKRGGASVDIK-----158		
Qy 354 GMEGTLPLRNALGSYTA-----VAGVIG-AMVFSNPSAALYLTEDSGNTAEAKDGP 405		
Db 159 SIEGKINK-AIEEPYQKPKSPFNTVTVKTLGQETTLDNKNEINLSEDKVQNTA-----211		
Qy 406 GPSFNRFYCOAGPHALAANQTDRGHVLSSQSTGSNTTBEFSYDYLALICGFGAPILLRL 465		
Db 212 ---NIDYRIVGNOLVLT-----NSNSKGTLTKKSAGTGTGTP-VAYK 251		
Qy 466 FYLERCDAGAFTGGHGDALKYVTCGTFDSEIPCSLCEHRTRPVCAHTVHRLRORMRFRGQ 525		
Db 252 AGLQTVMAGLDKENTVAKTINYETKGS-LKLKIDKEGSPDLYPTVFL-----DFGK 304		
Qy 526 A-----TROPIQGVFGTMNSQYSDCPDLYNYA-----PYLLRKXPGDOTEAAKATM 570		
Db 305 ALPSKDVDTDKDGTI-----SILDGIPNGTKYTITERSVDPDPMIDTPMATTAKGETI 358		
Qy 571 QDTYRATLRLRFLDQEERLLDRGAPCSSEGSL-----SVIDHPTP-FRRLDTLRA 621		
Db 359 SMTSKNMVKRGQGQILLEKTG-VERGTDLWNNTSLAGNTFAIRKDSPACEIVQBTIDEGK 417		
Qy 622 RIEBTTTQPMKVLTVERDVKIRELSEATHSMALTFD-----YSGAFCPTTFNLFYKTR 675		
Db 418 RAB-TPKELANALELGTYVTE-TKNSNGFTNTFKPTEKVELKYAQTVAUTSNVTKQ 473		
Qy 676 HLAVIDQDIL-----SQCHCVFYGQV-----EGRNFRNQFQPVYLRRFVLD 717		
Db 474 NOB1GETTILKEDKDGTGESESQKAETYLFTAKDQGAVKWSAFK-----TEL 526		
Qy 718 FNGGP1S1S1T1V1S1B-GPVSAPNPTLQ-----DAPAGRTFPGDGLARVSVE-----764		
Db 527 VKGETKASDTEVTLALDEKNOVAVKHLAINEYFWQETKAPEGTYLDETKYPSIKVYDNNE 586		
Qy 765 -----VTRDTRVQKV-----FSGNTNLSSEA-----RARLVGLASAYQDQEER 805		
Db 587 KNAVITRDTIATKEQVIRGFDKEFKFAGSADGTAETGFDLSKPSVPLEGTXEITGAEDKA 646		
Qy 806 VDMLHGLALGF-----LLKQFHGLLFPGRM-----PPNSKS-----PNP 838		
Db 647 TTANEQLQFDGKGFENPYGDLLESEA-----PEGFQKIPLEIRSTFKENKDDYAKS 703		
Qy 839 QWFNTLQLRNQ-----MPADKLTHPEBTTIAAVKRFTEEYAAATNFNLP-PTCIGE 888		
Db 704 EYVFTTBSQKQPKMVTVPYKELTNN-----FVSILNRNLMLDPEKEDSLTS 754		
Qy 889 LAQFMAMNLJLKYCDHSQQLINWTSITGARRPRDPSSVLMWIKD-----WTSAAAD1ETQ 945		
Db 755 LATWDGNKCLNTDFTE-LVDKL-----RYNLHEIKEDWVVAQAIYDEA- 799		
Qy 946 AKALLEKTNLPMLMTATST-----HLVRAAMNQRPVWVIGLISISKYHGA 992		
Db 800 TKAQEKDQKAKPVIWIAETTATLANKETGTMKTLHKLTAEQ-----VLDKSV1FVN 853		
Qy 993 AGNNRVPQAGNWGLNGGKVNGLNGKVNGLPLFTDRTRFTIACPRGGFCICPTGPSSGNRETTLSD 1052		
Db 854 YENKVAEAGNE-----PVA-----		
Qy 1053 QVRGIVSGAMVQIAATVTVRANGER-----AQMAFDWLSLTDDEFELARDL- 1102		
Db 876 QAQ-----TWNCTIERHVSQTQKAHLEDGSQTFTSDVMDMFDDSVTHVLD 923		
Qy 1103 -BEELHDQIQTQLETPWYEGALBAVKTIDE-----KTTAGD-----GETPTNLAFFKEF- 1149		
Db 924 GSKEAEFTTLYALIDGDTKNEIWKGKLEHEVNDKEFVTKLAEKDVKYPESTKEF- 982		
Qy 1150 SCEPSHDTISNV-----LNISGSNISGSSTVPGLKRPEDDE 1185		
Db 983 -TEINYEKOGNVNGKHINEDLKEKSQTLTPEKVPTRIPSTPKOPE 1024		
RESULT 11		
US-10-206-57-394		
Qy ; Sequence 394. Application US/10206576		
Db ; Publication No. US2003001745A1		
Qy ; GENERAL INFORMATION:		
Db ; APPLICANT: Choi et al.		
Qy ; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides		
Db ; NUMBER OF SEQUENCES: 497		
Qy ; CORRESPONDENCE ADDRESS:		
Db ; ADDRESS: Human Genome Sciences, Inc.		
Db ; STREET: 9410 Key West Avenue		
Qy ; CITY: Rockville		
Db ; STATE: Maryland		
Qy ; COUNTRY: USA		
Db ; ZIP: 20850		
Qy ; COMPUTER READABLE FORM:		
Db ; MEDIUM TYPE: CD-R		
Qy ; COMPUTER: Dell Latitude		
Db ; OPERATING SYSTEM: Windows 98		
Qy ; SOFTWARE: ASCII Text		
Db ; CURRENT APPLICATION DATA:		
Qy ; APPLICATION NUMBER: US/10/206,576		
Db ; FILING DATE: 29-Jul-2002		
Qy ; CLASSIFICATION: <Unknown>		
Db ; PRIOR APPLICATION DATA:		
Qy ; APPLICATION NUMBER: US 09/071,035		
Db ; FILING DATE: 1998-05-04		
Qy ; ATTORNEY/AGENT INFORMATION:		
Db ; NAME: Hyman, Mark J.		
Qy ; REGISTRATION NUMBER: 46,789		
Db ; REFERENCE/DOCKET NUMBER: PB369P1D1		
Qy ; INFORMATION FOR SEQ ID NO: 394:		
Db ; SEQUENCE CHARACTERISTICS:		
Qy ; LENGTH: 1074 amino acids		
Db ; TYPE: amino acid		
Qy ; STRANDEDNESS: single		
Db ; TOPOLOGY: linear		
Qy ; MOLECULE TYPE: protein		
Db ; SEQUENCE DESCRIPTION: SEQ ID NO: 394:		
Qy ; Query Match 2.0%; Score 123; DB 12; Length 1074;		
Db ; Best Local Similarity 18.3%; Pred. No. 0.078;		
Qy ; Matches 206; Conservative 150; Mismatches 415; Indels 352; Gaps 52;		
Db ; RTTSLIAETNGAKQTFC-IEPGVSIPTVHG-----QKNPL 104		
Qy 250 RVRNTAVARGAAHLADEFENHEGAVLPPDITYTYFQSSSSGGTTARGARRNDVNSTSKPS 309		
Db 67 RTTSLIAETNGAKQTFC-IEPGVSIPTVHG-----QKNPL 104		
Qy 310 PSGCFERRASIM-AADTALHAEVTLNGTIVEE-----TPTDIREKWPMPFI 353		

US-10-282-122A-45763 ; Sequence 45763, Application US/10282122A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Lianguo  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlson, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Frwick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Porwitz, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELTRA 034A  
; CURRENT APPLICATION NUMBER: US/10/282 122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,525  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 7814  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 45763  
; LENGTH: 2358  
; TYPE: PRT  
; ORGANISM: Bacillus anthracis  
US-10-282-122A-45763  
Query Match Score 1.9%; Score 121; DB 12; Length 2358;  
Best Local Similarity 18.7%; Pred. No. 0; 5; Indels 464; GADS 65;  
Matches 266; Conservative 178; Mismatches 517; Entropy 153  
Db 520 TFTSSLAVSGARTGLAGAGITIKLISHFYPVSVFHGGKHLPESSAAPNLTRACNA 116  
Qy 57 TFTSSLAVSGARTGLAGAGITIKLISHFYPVSVFHGGKHLPESSAAPNLTRACNA 116  
Db 575 SATFTTPVQGQQPSGOATSNTVTTINADIRTRKIVDRAFATVNDLTVTTIENTG 634  
Qy 117 RERFSSRCG-PPVDG---AVBT- GAEICTRIGLEP-----ENTI 153  
Db 154 LYLVVTAFLPKBAVMNCNVPHYGGDIDVHNGDVRVPLFPYQLMFDVNRLYPDPFNT 213  
Qy 635 NVLATNNVFQDPPIPQTTFI-TNSVTVGVSQPGANPATGFTVANISPGGSRIV-TTFCQV 691  
Db 214 HRSIGEGFVYPTPPFTNTGLCHLHDVCAPIVMAVAYRVN---VTAVARGAHLLAFDE 268  
Qy 692 RVTSPSGGTIP---NRG-NVTANFVVIPTQNPPTINQNTNTVVTQNTGGLNVIKEY 745  
Db 269 NHEGAVLPPDITYT-----YFQSSSS-----GTTARGARRNDVNNTSK 307  
Db 746 NTTQAVGDTLTYTIAVQNTGNVPLNVEQDAISSAVSFVANSVTINGVPQSGLN-----801

Db 105 PMSDRAKULSVLNKEAGTIDIDTNNAQKRMIIWEVNGYKLRSKRLGASAVIDK-----158  
Qy 354 GMEGLIPRNLALGSYSTAR-----VAGVYG-ANVPSNSALYLTVEEDSGMTAEKDGGP 405  
Db 159 SIEGKLINK-AIEEYQKPKPFHNTVKTGQSTLIDNEELNSEDFKVQNTA-----211  
Qy 406 GPSFRFYQTAGPHIAANPQTDRDHVLSQSTGASNTTFSVYDYLALICGFGAPLLARL 465  
Db 212 ---NDYRIVGNQLVLT-----NSNSKGTLTLLKKSAGTGTGTP-VAYKK 251  
Db 466 FYLERDAGATTGAGTGGHDALKYVGTGTDSEPCSLCSEKTRPVCAHTTVERLORMPRGQ 525  
Qy 252 AGLOTMAGALDKPNTYAIKINVTKGS-LKIKIDKESSDIVPBTVFLU-----DGK 304  
Qy 526 A-----TROPIGVFTMNNSQSDCDPLGHNYA-----PYLILRKPGDQTEAAKATM 570  
Db 305 ALPSKDVUTTDKG-----SILDGPFGKTVTTEKSVDPMIDTTPMANTKAGETI 358  
Qy 571 QDTYRATLERLFLDIBERLLDRGAPCSSIGLS-----SIVIDDHPT---FRRILDTLRA 621  
Db 359 SMTSKNMRQCGOILLERKG-VETGTDLWNNSYSLAGNTFAIRKDSPAGEBTVQEITTDKG 417  
Qy 622 RIEQTTTQFMCVLUVERDYKXREGLSATHSMALTFD-----YSGAFCRBTINFLWVKT 675  
Db 418 RAE-TPKELANALELGTYYKTE-TKSSNGFVNTEKPTVKELYKANOTVLTNSVVKCQ 473  
Qy 676 HLAVVQDOL-----SQCHCYFVGQOV-----EGRNPRNQFPVPLRRRFVDL 717  
Db 474 NOEITGETTITKEDKDTGNESQSKAFKGKGEYTLTAKDQAVKXSEAK-----TSL 526  
Qy 718 ENGGFISTRISITVTLSE-GPVSAPNPTLQQ-----DAPAGRFTGDLAVPSV-----764  
Db 527 VKGTKASDEVTILALDEKKNVQAVKHLAINEFWQETKAPOGTYLDETKVSVIJKVDNNE 586  
Qy 765 ---VTRDITYKTRVY-----FSGNCNTNLSEAA-----RARLVGLASAYOERK 805  
Db 587 KNAVITDVTAKEQVTRFGDFEKFGASDCTAETGENDJSFKVSPLEGKXETGAEDKA 646  
Db 806 VDMLHGLGF-----LJKQFHGLLPPGM-----PPNSKS-----PWF 838  
Qy 647 TTACNEQLGFDGKGPKENLYPGDYLLEBIEA--PGFQKITPLERSTFKENKDYAKS 703  
Qy 839 QWFWLQRNQ-----IMPADKLTUEETTIAAVKRFEBYAAINFNLP--PTCIGE 888  
Db 704 EYFTTIEEGQKOPIKNVTVPYKELTNNE-----FSYSLNNLMLYDPEREDSLRS 754  
Qy 889 LAOFYMANLILKCYDHSOYLINTLTSITGARRPDESITHWIRD---VTSAADEIQ 945  
Db 755 LATWDGKRNLTDFE-LVDKL-----RYNHIEKEDWYVQAIDVEA- 799  
Qy 946 AKALLEKTEENLPELWTAFTST-----HLVRALMNORMRPMVYGISISKYHGA 992  
Db 800 TKAQEQKDKEAKPVVIASTTANKEKTYWKLHLKTAEQ-----VLDKSVLFTNY 853  
Qy 993 AGNNRVOQGMNSLNGKNCVPLFTDRRFRFIACPRGGFICPYGPGSSGNRETTLS 1052  
Db 854 YENKVAEAGNE-----PVA-----RDASLNN 875  
Qy 1053 QTRGILVSGGAMYQLAYTIVRAGAR-----AQHMAFDWDWLSLTDPDEFARDL- 1102  
Qy 926 QPQ-----TWNCTIERHVSLOTKAHLEDGQTFHGDVNDMFDVSVTHDVLQ 923  
Db 876 YENKVAEAGNE-----PVA-----RDASLNN 875  
Qy 1103 -BELHDQIQTLETPTWVGEALEAVKILDE-----KTAGD---GEPTNLAFNFD 1149  
Db 924 GSKEBAFETILYALLPDGTNKEIMKGKSLIEVNDKEFTKTYLAEKVDTGKYPEGTKFTP- 982  
Qy 1150 SCFPHDHTTSNV-----LNISGSNTSGSTPGGLKRPPDE 1185  
Db 983 -TEINYKDGNVNGKHNEDLKERSQTLIPEVPTIPSTPKQFE 1024

308 PSEGGPFERLASMAADAL-----HAEVFN----TGYTEETPDIKEWPMF 352  
 802 -PNTGFS -LPNTPAAQTVVTFDVLIIQDPNEDILQANVTAQVNFS- -EPPVT 854

353 IGM-----EGTLPLRNALGSYTAVAGYIGAMVFSPSNALSALTEVEDSGMTEAKD 402  
 855 INVSNIVNTVQGNFPEVKSYNTDVAVGDFV-----VYIEVIAAGSV---- 900

403 GGPSPSFNFYQGP-----HLAANFOPTDRDGHVLISSQSTGSS---NT 443  
 901 - - - - -PATNSNIVNTVQGNFPEVKSYNTDVAVGDFV-----GFPDLPLPGASIVTVF 953

444 EFSYDYLALICGSPAPLLFLYERDAGATGGHDALKVYTG-----DSEIPCSIC 500  
 954 EVLIDEIPU-----GNNVYNSANVNTGDFLFLNPTEPPTV 988

501 EKHTRPVCAHTTVERLQIMPRFGQATR-----QPIGVGTMQSYQSDCDP 547  
 989 EPNTV-----TVVNSGIVNIKVSQATEAGVGDITLYTVRQNSGTVFAATNVSEJLIPS 1045

548 GN--YAPYJILR-----KPGDQTEAAKATMODYTATLRLFLIDQERLRDLGA--- 595  
 1046 GTTFWVNTSYINGTPQPGNIPTCFLANIPVSGMVTYAFQVITSYSPNPNVLPNANVT 1105

596 -----PCSEBGLSSVIVDHP----TFRILDTLARIEOTTOFEMKYLVETR-- 638  
 1106 ADFOVSPLPPIPITVNTVIRVNVGSSLNVMSKVNVLQAGVGDITL--VTLIGNTGT 1163

639 -----DVKIREGLSEATHSMALT----FDPYSGAFCPTNFLVKRTHLAVQDLA 684  
 1164 VPATNIIFDPPIPEGTAVANSTVQVQGADPMAG--FPVNPNTVPGQTATVTFQ-- 1218

685 LSQTHCVPNGQQVGRNPNQFQ-----PVLRFRFDLNGFFTSSTRSITVTL 732  
 1219 - - - - -VTTISIPEGGNTRNQSNITASFLINPANPPI----TTVNTSNFVVTQVNTAQL 1267

733 SEGVVSAPNPTLGDAPIRTF-----DGDILARVSVEVDIR----VGNRUVFSG 779  
 1268 NIQKTSVV-----QQAALGETTYSVSVIRNNGTVATATNSFIDPIAPBTYVANSTTING 1322

780 -----NCTNLSEAAARLVLGLASAYQ-----800  
 1323 TPQGFDPTVGFPLNIAAGTSLTVFQTVIAPISTRGAVLNTASAATFLNPLQBPVT 1382

801 -----ROEKRYDMHNGALGELIKOFHGHLLFPRGMPPNSKSPNFW 840  
 1383 TTNSNTTVTIPPLPPGGTATKTVDAAGA/GDVL-TYTTLISNGIIPV-----

841 FWTLLQRNOMPADKLTHEITTAALKRFTEEYAAINFLNPLPTCIGELAQFYMANLILK 900  
 1435 -DVFQDVTPEGTPEVGSVTTGGVQOGLN-PEIGTTVPLIAGSSEIBTQFTITE 1491  
 901 YCDHSQYLNTLTSITGARRPRDSSV-----LHWIKDVTSAAD 941  
 1492 IPD-NEVILNDAVDTFTSQNPQEPPTITLNLVVTINIAFVFPKLVDKEVATVGE 1550  
 942 IETOQAKALLEKTEENLPELTTAFTSTHLVRAAMNQRPVHLGISYKHAAGNNRVEQA 1001  
 1551 ILTV-DVLLFNGFTV-----ATVQYSDVLPSSIAFPNSVTDGYLQP 1594  
 1002 G-----NWSGLNGGKNTVCPFLFTDRAFRFIAACPRGFICP-----1037  
 1595 GFNPANGFPLPDIINGEST- -EVTFQVT---VIVSPNSNGTIVTANTVGSFLVPGEPVV 1649  
 1038 -VTGPSSGNRBTTLSDQV9GIIIVSGGAMVQIAIYATVRAVGARACHIAFDDWLSLTJDE 1096  
 1650 IVTGESN-----TTLTTVNG-----QFNTIKQVNRRAATLGDVLTIVYQITNT-GT 1695  
 1097 FLARDLBEDHQIQTLE-----TPWTEGAEALKIDETTGTGDETP----- 1141  
 1696 VTAIVV-----QFDTISAGSFVNSVTINGALQ- -PNLNPITGFVGDIPVGETVWTT 1748  
 1142 -----TNLAFNFDSEPSHIDTSNVLNSGSN1SGSTVPLKRP 1181

Db 1749 FQATVNTI-----PASGTITVNTVNTG---SCTLYVFG- -EPP 1780

RESULT 13  
 US-09-905-129-2  
 Sequence 2, Application US/09005129  
 Patent No. US20030137705A1  
 GENERAL INFORMATION:  
 / APPLICANT: Binn, et al.  
 / TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF  
 / FILE REFERENCE: 540579-2007.2  
 / CURRENT APPLICATION NUMBER: US/09/905,129  
 / PRIOR FILING DATE: 2001-07-13  
 / PRIOR APPLICATION NUMBER: 09/802,318  
 / PRIOR FILING DATE: 2001-01-08  
 / PRIOR APPLICATION NUMBER: 60/207,821  
 / PRIOR FILING DATE: 2000-05-30  
 / PRIOR APPLICATION NUMBER: 60/084,944  
 / PRIOR FILING DATE: 1998-05-11  
 / PRIOR APPLICATION NUMBER: 60/085,673  
 / PRIOR FILING DATE: 1998-05-15  
 / NUMBER OF SEQ ID NOS: 25  
 / SOFTWARE: Patentin version 3.0  
 / SEQ ID NO: 2  
 / LENGTH: 2597  
 / TYPE: PRT  
 / ORGANISM: rattus species  
 / FEATURE:  
 / NAME/KEY: misc. feature  
 / LOCATION: (1)..(2597)  
 / OTHER INFORMATION: 'x' can be any amino acid  
 US-09-905-129-2

Query Match 1.9%  
 Best Local Similarity 18.6%  
 Matches 145; Conservatve 113; Mismatches 287; Indels 233; Gaps 40;

Db 274 SGAFLCTKPTIDPSLKSLSLVTQDNGSASTSPDFTIEPFGSLSLINTMTXSGNKAADMVCS 333

Qy 416 AGPHLAPNQTD--RDGHVLSQSTGSSNT-----FSVVDYLALIGC 455  
 Db 334 1QKP-----SETSPTAFFTEENDYIM- -INASPTSTMVLCVSDYNNHQPVWQVLLALYS 382

Qy 512 TVHRLRQMRP-----RFGQATRQPIGVFGTMNSYSDCDPGLGNTAPYLRLRPGD 561  
 Db 383 DPLIIEKQOLTEPSSRKYQVALRFDIPEPSIDEAVR- -APFWFQEKIVLQLART 441  
 Qy 456 FGAPLARLFLYERDAGATGGDALKYVTFDPSLCLCERKTRPV---CAHT 511  
 Db 334 1QKP-----SETSPTAFFTEENDYIM- -INASPTSTMVLCVSDYNNHQPVWQVLLALYS 382

Qy 562 QTEAAKATMDTYRATLERFLDQEQLR-----LDR-----GAPCSSEG 601  
 Db 442 ATTLSLQIQFSTDQIAQIALPRAEVRAERLKWTMILMNPKLERTVLYVGTIAISPGKGS 501  
 Qy 602 -----LSSVYDHPFR-----RILDILTRARIE- -CTTQENPKV-----VETD-----639  
 Db 502 DPSPHLWLLADGSKTRAPVSEDRFLIDRNGKLELQADSPDAGLYHCISTNDADADV 561  
 Qy 640 -YKIR -EGISEAHTSMALTDPSYGAF---CPIITNLVKGTHLAVYDLSLQCHCV 691  
 Db 562 LTYRATVVEPBPYGEESTDSGQHTVYGETDLPLCSTG-----VTDASIS- -WT 608

Qy 692 PYQQQVEGRNFRNQFQPVLERFVDFLNGCFISTRSTIYTLSGPVS - APNPT-----743  
 Db 609 LPGNTVFSOPERDR-----QILNGNTLRLQVT- -PKDQGHYQCYAANPSGADFSS 657

Qy 744 -----LGQDAPASRTFEDDLARYSVEVIRVKNRUVFSGNNTNLSEARAR 791  
 Db 658 FKVSVOKKGQRMVDEAEGGSLGE- -PNSVSVLKQPAULK-----LSAALTGSEAGKQ- 711  
 Qy 792 LVGLASAYOREKRYDMLHGALG- -FLKQFHGLLFRGRMPNSKSPNPWFWTLLQ- -R 847

712 ----VSGVERKNGRDLTHRRGDESTLRRFRE -HRROLPLSARRIDPQRWALLEKAKK 765  
 848 NQMPADKLTHEETT----IAAVKPFTEYRAINFNLPPTCIGELAQFYMANLILK 900  
 766 NSV----KQENTTKVPKPVLAYPLVELTDEEKAQNM----P----- 802  
 Db 901 YCHSQYLINTLTLITGARRPRDPSSVLIWIRKDVTSAADETQAKALLETENLPELW 960  
 Db 803 -DEEFMLKTKASGVPGESPTADSGPYNHGENFTSIASTGETVSTVNQTLQ-SEHLPDFK 859  
 Qy 961 TTAFTSTHILVRAAM----NORPMVYLGISIISKYHGAAGNNRVRQAGNNG-- 1006  
 Db 860 LFSVTINGTAVTKSNPSIASKIEDTTNQPLIIFP-SVAEIRDSA----QAGRASSQS 912  
 Qy 1007 -LNGKRNVCPLFTEDTRTRFLTACPRGGFI-----CPVTG --PSSGN 1045  
 Db 913 AHPVYGGN----MAYGHTNYYSETSKASTVLIQPINPTESYGPQIPITGVSRSQSSD 966

RESULT 14  
 US-09-905-129-10  
 ; Sequence 10, Application US/09905129  
 ; Patent No. US00201377105A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Birat, et al  
 ; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: 5405779-2007.2  
 ; CURRENT APPLICATION NUMBER: US/09/905,129  
 ; CURRENT FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: 09/802,318  
 ; PRIOR FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: 60/207,821  
 ; PRIOR FILING DATE: 2000-05-30  
 ; PRIOR APPLICATION NUMBER: 60/084,944  
 ; PRIOR FILING DATE: 1998-05-11  
 ; PRIOR APPLICATION NUMBER: 60/085,673  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 2597  
 ; TYPE: PRT  
 ; ORGANISM: Rattus sp.  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(2597)  
 ; OTHER INFORMATION: 'x' can be any amino acid  
 US-09-905-129-10

Query Match 1.9%; Score 120.5; DB 9; Length 2597;  
 Best Local Similarity 18.6%; Pred. No. 0.67%; Mismatches 113; Gaps 40;  
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;  
 US-09-905-129-10

Qy 416 AGPHLAANPQTD--RDGHVILSSQSTGSSNTE-----FSDYLAJCG 455  
 Db 274 SGAFICLKTPIDPSLKSRSKLVTDNGSASTSPQDFIPFGSISLNNMXXSNTADNVC 333  
 Qy 456 FGAPLLARLFLYLERCDAGFTGGHDAKYVGTGDFSEIPCSLCEKTRV--CAHT 511  
 Db 334 IQKP-----SRTSPATPEEENDYM-LNVAFSNTLVCSVDYNEHQIPWQMLALYS 382  
 Qy 512 TVHXRORM-----RFGQATRQTPSLSSRYQVALRBDIFTSIEADVR-ADPFWQKEKVLQLNRT 441  
 Db 383 DSPLLERKQHLETPSLSSRYQVALRBDIFTSIEADVR-ADPFWQKEKVLQLNRT 441  
 Qy 562 QTEAAKATMDTYRATLERFLIDLEQERL-----LDR-----GAPCSSEG 601  
 Db 442 ATTSLTQLQIFSTQIAFRAEDRAEIKWTHMLMMANPRLERTVYGGTIALSCPGK 501  
 Qy 602 ----LSSV1VDHPPTFR-----RILDTRLARIE-QTTQFMKV-----VETRD----- 639  
 Db 502 DPSPHLEWILADGSKVRAPYVSEDRILLDNGKLEONADSFDAGLYHC1STNDADAV 561

Qy 640 --YKTR--EGLSEATHSMALTFDPYSGAF---CPITNFLVKRTHLAVYDODLALSOQHCV 691  
 Db 562 LTYRITYVEPYGESTHDQVQHTVVTGFTDLPCLISTG-----VPDASIS-WI 608  
 Qy 692 FYQQOVBGRNFRNQFOPVLRFFRVDLNGFISTSITVTLSEGFSV--APNPT---- 743  
 Db 609 LPGNTYVSOPSRDR-----Q-LNNNTLRLQVT -PDQGHYQCYAANPSEADFSS 657  
 Qy 744 -----LGQDAPAGRTEDGLARYSVEVIRDIVYKRNVYSGNTNLSEARAR 791  
 Db 658 FKVSVQKGQRMVEHDEAGSGSGLGR-PNSSVSLKQPSALK----LSASALTGSFAGKQ- 711  
 Qy 792 LVGLASAYQREKRDMLKGALG-FLIKQPHGLPPRGPNKSPNPQWFTWLLQ--R 847  
 Db 712 --VSGVHRENKRNKHDLIHRRGDSTLRRRE--HRROLPLSARRIDPQRWALLEKAKK 765  
 Qy 848 NQMPADKLTHEITT----IAAVKPFTEYRAINFNLPPTCIGELAQFYMANLILK 900  
 Db 766 NSVP---KQENTTKVPKPVLAYPLVELTDEEKAQNM----P----- 802  
 Qy 901 YCDHSQYLNLTTSITGARRPRDPSSVLEWIRKDVTSAADETQAKALLETENLPELW 960  
 Db 803 -DEEFMLKTKASGVPGESPTADSGPYNHGENFTSIASTGETVSTVNQTLQ-SEHLPDFK 859  
 Qy 961 TTAFTSTHILVRAAM----NORPMVYLGISIISKYHGAAGNNRVRQAGNNG-- 1006  
 Db 860 LFSVTINGTAVTKSNPSIASKIEDTTNQPLIIFP-SVAEIRDSA----QAGRASSQS 912  
 Qy 1007 -LNGKRNVCPLFTEDTRTRFLTACPRGGFI-----CPVTG --PSSGN 1045  
 Db 913 AHPVYGGN----MAYGHTNYYSETSKASTVLIQPINPTESYGPQIPITGVSRSQSSD 966

RESULT 15  
 US-09-905-129-13  
 ; Sequence 13, Application US/09905129  
 ; Patent No. US20020137705A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Binat, et al  
 ; TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREI  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/905,129  
 ; CURRENT FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: 09/802,318  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/207,821  
 ; PRIOR FILING DATE: 2000-05-30  
 ; PRIOR APPLICATION NUMBER: 60/084,944  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 2597  
 ; TYPE: PRT  
 ; ORGANISM: Rattus sp.  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(2597)  
 ; OTHER INFORMATION: 'x' can be any amino acid  
 US-09-905-129-13

Query Match 1.9%; Score 120.5; DB 9; Length 2597;  
 Best Local Similarity 18.6%; Pred. No. 0.67%; Mismatches 113; Gaps 40;  
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;  
 Db 416 AGPHLAANPQTD--RDGHVILSSQSTGSSNTE-----FSDYLAJCG 455  
 Qy 456 FGAPLLARLFLYLERCDAGFTGGHDAKYVGTGDFSEIPCSLCEKTRV--CAHT 511  
 Db 334 IQKP-----SRTSPATPEEENDYM-LNVAFSNTLVCSVDYNEHQIPWQMLALYS 382  
 Qy 512 TVHXRORM-----RFGQATRQTPSLSSRYQVALRBDIFTSIEADVR-ADPFWQKEKVLQLNRT 441  
 Db 383 DSPLLERKQHLETPSLSSRYQVALRBDIFTSIEADVR-ADPFWQKEKVLQLNRT 441  
 Qy 562 QTEAAKATMDTYRATLERFLIDLEQERL-----LDR-----GAPCSSEG 601  
 Db 442 ATTSLTQLQIFSTQIAFRAEDRAEIKWTHMLMMANPRLERTVYGGTIALSCPGK 501  
 Qy 602 ----LSSV1VDHPPTFR-----RILDTRLARIE-QTTQFMKV-----VETRD----- 639  
 Db 502 DPSPHLEWILADGSKVRAPYVSEDRILLDNGKLEONADSFDAGLYHC1STNDADAV 561

RESULT 16  
 US-09-391-630-2  
 / Sequence 2, Application US/09991630  
 / Patent No. US200201514A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Einat, et al.  
 / TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCED  
 / CURRENT APPLICATION NUMBER: US/09/991,630  
 / CURRENT FILING DATE: 2001-11-06  
 / PRIOR APPLICATION NUMBER: 09/05/129  
 / PRIOR FILING DATE: 2001-07-13  
 / PRIOR APPLICATION NUMBER: 09/802,318  
 / PRIOR FILING DATE: 2001-03-08  
 / PRIOR APPLICATION NUMBER: 09/729,485  
 / PRIOR FILING DATE: 2000-12-04  
 / NUMBER OF SEQ ID NOS: 28  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO: 2  
 / LENGTH: 2597  
 / TYPE: PRT  
 / ORGANISM: Rattus species  
 / FEATURE:

Qy 456 FGAPLLARLLPFLERCDAAGFTGHDALKYVGTGFDSEIPCSLCEKTRPV---CAHT 511  
 Db 334 IQKP------SRTSPTAFTBENDYM---LNSAFTSNLVCSYDYNH1QPVNQMLALYS 382  
 Qy 512 TVFLRQMP-----RFQATRQPIGFGTMSQYSDDPGNYAPYLIRKPGD 561  
 Db 383 DSFLIERKPOLTTETPSLSSRYQVALPEDITSIEADVR-ADPFWQQEKLVLQUNRT 441  
 Qy 562 QTEAAKATMODYTTRALFLDIEQERL-----LDR-----GAPCSSEG 601  
 Db 442 ATTSLTQIQFSTDQIAQIPRAEMRAERLKWTMILLMANPKLERTVNGGTIALSPGKG 501  
 Qy 602 -----LSSSIVVDPHTER-----RILDTLRARIE-OTTQTMKVL---VETRD---- 639  
 Db 502 DPPPHLWLLADESKVRAPIVSEBDGRLIDKNGLLELONMADSFDAGLYHC1STNDADADV 561  
 Qy 640 -YKIR--EGLSEATHSMALTFDPYSGAF---CPIITNFLYKERTHLAVYQDIALSOCHCV 691  
 Db 562 LTYRITVYEPYGPGSTHDSGCVQHTVTGTDLPLSTG-----VPDASIS---WI 608  
 Qy 692 FVGGQVGEGRFRNQFQPVJRRRFVTDLFNGCPISTRSTITYLSECPVS---APNPNT---- 743  
 Db 609 LPGNTVFSQPSRDR-----QILANGTLRLQVTT-PKDQGSHYOCVAANPGADFSS 657  
 Qy 744 -----LGQDAPAGRTFGDPLDARVSVETVDRVKNRVVFSGRGTNUSEAAAR 791  
 Db 658 FKVSVQKQGMRVTEHDREAGGSLGE-PNSSVSUKQPSLX-----LSASALTSEAGRO- 711  
 Qy 792 LVGLASAYQROEKRVDMLHGALG\_FLLKOFHGGLPGRMPPNSKSNPONWFHLLQ---R 847  
 Db 712 -----VSGVARKNGHDL1HRRGSTDPLFRE--HRRQDLSAARIIDPWRWALLEKAK 765  
 Qy 848 NQMPADKLTHEETT-----IAAVKRFTEEYAAINFNLNPLPTCIGELAQFYMANLILK 900  
 Db 766 NSVP-----KKOENTTIVKPVPLAVLVEATDEEKAQSGM---PP----- 802  
 Qy 901 YCDVHSQIINTLTSITGARRPDRPSVWIRKDVTSASADIEQKALLEKENTPEIW 960  
 Db 803 --DEFEMVILKTRASGPGRSPADSGPVNHFGMTSISASGETEVNTNPQTLQ--SEHLPDFK 859  
 Qy 951 TTAFTSTHLVRAAM-----NQRPMVVLGIGTSKRYHAGNMRVFOAGNSMSG-- 1006  
 Db 860 LFSYVNGDPAVTKSMPBIAKLETTNQNPB1PP-SVAEIRDSA-----QAGRASSQS 912  
 Qy 1007 ---LNQGGKVNCPPLFTDFTRTRFLIACPRGFFI-----CPVYTG--BPSGN 1045  
 Db 913 AHPVYGGN---MATYGHNTYSSFTSKASTVLOPINPTESYGFQIPTGVSPFSSSD 966

NAME/KEY:	misc_feature	Score: 120.5;
LOCATION:	(1..(2597))	Pred. No. 0.67
OTHER INFORMATION:	'x' can be any amino acid	Mi smatches
US-09-391-630-2		
Query Match	1.9%	Score: 120.5;
Best Local Similarity	18.6%	Pred. No. 0.67
Matches	145;	Conservative
Db	416 AGPHLAANPQTD--RDGHVLLSSQTGSNSNTE--	
Qy	274 SGAFLCTRKPTIDPSLKSLSLVTOEDNGSASTSPQ	
Db	456 FGAPFLARLLFYLERCDAGAFTGGGDALKVTVTG	
Qy	334 IQRH--SRTSPTAFTEEENDYIM-LNAA	
Db	512 TVHVLRQRMF-----REFQATROPIQGVFG	
Qy	383 DSPHLERKPLQITTPSLSSRYKQVALRPDIFT	
Db	562 QTEAKATMQDTYRATLRLFIDLEQERL-----	
Qy	442 ATTLSLTLQQLQSTAAQIALPRAEMAEERLKWTMIL	
Db	602 -----LSSVIVDHPTRF-----TRILDTRAR	
Qy	502 DPPSHLEWLLADGSKVRAPIVYSEDGRILLDKNGK	
Db	640 --YKIR--EGLSEATHSMALTFDPSGCAF---C	
Qy	562 LTVITITVVPYGESSHDSGIVQHTTVVGETLDLPC	
Db	692 FGQQQVEGENRPNRQFQPVLRRFVFLNGGFISTH	
Qy	609 LPGNTVFSQPSRDR-----QILNNNTLRLI	
Db	744 -----LGODAPAGRTFDGDLARYEV	
Qy	658 FKVSVQKGORMVHEDREAGGSGLGE--PNNSSVSLL	
Db	792 LVGLASAYORQEKRVDMLHGALG-FULLQFHGLLL	
Qy	712 -----VSGVIRKNGKHDHLIERRGDSLRRFRE-1	
Db	848 NQMPADKLTHEETIT-----IAAVKRFTEBYAA	
Qy	766 NSVP---KQENTTIVKPVPLAVPLVLTDEBEKD	
Db	901 YCDHESQYLINTLTSITGARRPDRDPSVSLWIRK	
Qy	803 --DEFMVKTKASGPGRSPTAQSPVNHGEMTIV	
Db	961 TTAFTSHTLVRAM-----NQRPMVVL	
Qy	860 LFSVNTGATVKSXNPSIASKIEDTNQNPIIIFI	
Db	1007 ---LNGGRNVCPLFPTDRTRFIAIQRGGFI--	
Qy	913 AHPVTGGN---MAYGHTNTYSSFTSKASTVYLO	
Db		



RESULT 19

US-10-454-351-2

Sequence 2, Application US/10454351

Publication No. US20040053301A1

GENERAL INFORMATION:

APPLICANT: Quark Biotech Inc.; Paz Einat, et al

TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF

FILE REFERENCE: 010\_PCT2-US2; EINAT=73

CURRENT APPLICATION NUMBER: US/10/454,351

CURRENT FILING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: US 09/931,630

PRIOR FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US 09/905,129

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 09/802,318

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 09/79,485

PRIOR FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: US 09/312,216

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 2597

TYPE: PRF

ORGANISM: Rattus species

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(2597)

OTHER INFORMATION: 'x' can be any amino acid

US-10-454-351-2

Query Match 1.9%; Score 120.5; DB 12; Length 2597;

Best Local Similarity 18.6%; Pred. No. 0.67%; Mismatches 113; Indels 233; Gaps 40;

Matches 145; Conservative 113; Mismatches 287; Length 2597;

Query 416 AGPHIAANPQD--RDGHYLSQPTGSNTE-----FSVDYLALIG 455

Db 274 SGAFLOTKPTIDPSKSKSLEYQEDNGSASTQDPIEFPGLSILNNTXXSGNKAIDYKS 333

Query 456 FGAPILLARLFLYLERCDAGAFTGGHDALKRXTVGFDFSDIPEPCSRKTRPV---CAHT 511

Db 334 IOKP-----SRTSPATTEENDYIM-LNAPSSTLVCSDYNHQPYWQLALYS 362

Query 512 TVHRLQMP-----RFGQATRPIGVFTGMNSQSYSDCDPLGNYTAPYLILRKPD 561

Db 383 DSPLIWERKFOLETTSSLSSYYKQVALRPEDIFTSIEADYVR-ADFWFQOEKIVLQLNRT 441

Query 562 QTEAAKATMODYTARLRLFIDOLERL-----LDR-----GAPCSESG 601

Db 442 ATTLSLTIQDQALPRAEMRERKWTMILMNPNLRLERTVLYGETIALSCPGK3 501

Query 602 -----LSSIVVDPHTPF-----RILDILRARI-EQTQEMKV-----VETD-----639

Db 502 DPSPHLEWLLADGSKYRAPYYSEDGRILIDNGKLEQMAEDAGLYC1STNDADAY 561

Query 640 --YKIR--EGLSBATHSMALTFDYGAF---CPITNFLYKRTHJAVVQDLSQCHCV 691

RESULT 20

US-10-454-351-10

Sequence 10, Application US/10454351

Publication No. US20040053301A1

GENERAL INFORMATION:

APPLICANT: Quark Biotech Inc.; Paz Einat, et al

TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF

FILE REFERENCE: 010\_PCT2-US2; EINAT=73

CURRENT APPLICATION NUMBER: US/10/454,351

CURRENT FILING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: US 09/931,630

PRIOR FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US 09/905,129

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 09/802,318

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 09/79,485

PRIOR FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: US 09/312,216

PRIOR FILING DATE: 1999-05-14

SEQ ID NO 2

LENGTH: 2597

TYPE: PRF

ORGANISM: Rattus species

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(2597)

OTHER INFORMATION: 'x' can be any amino acid

US-10-454-351-10

Query Match 1.9%; Score 120.5; DB 12; Length 2597;

Best Local Similarity 18.6%; Pred. No. 0.67%; Mismatches 113; Indels 233; Gaps 40;

Matches 145; Conservative 113; Mismatches 287; Length 2597;

Query 416 AGPHIAANPQD--RDGHYLSQPTGSNTE-----FSVDYLALIG 455

Db 274 SGAFLOTKPTIDPSKSKSLEYQEDNGSASTQDPIEFPGLSILNNTXXSGNKAIDYKS 333

Query 456 FGAPILLARLFLYLERCDAGAFTGGHDALKRXTVGFDFSDIPEPCSRKTRPV---CAHT 511

Db 334 IOKP-----SRTSPATTEENDYIM-LNAPSSTLVCSDYNHQPYWQLALYS 362

Query 512 TVHRLQMP-----RFGQATRPIGVFTGMNSQSYSDCDPLGNYTAPYLILRKPD 561

Db 383 DSPLIWERKFOLETTSSLSSYYKQVALRPEDIFTSIEADYVR-ADFWFQOEKIVLQLNRT 441

Query 562 QTEAAKATMODYTARLRLFIDOLERL-----LDR-----GAPCSESG 601

Db 442 ATTLSLTIQDQALPRAEMRERKWTMILMNPNLRLERTVLYGETIALSCPGK3 501

Query 602 -----LSSIVVDPHTPF-----RILDILRARI-EQTQEMKV-----VETD-----639

Db 502 DPSPHLEWLLADGSKYRAPYYSEDGRILIDNGKLEQMAEDAGLYC1STNDADAY 561

Query 640 --YKIR--EGLSBATHSMALTFDYGAF---CPITNFLYKRTHJAVVQDLSQCHCV 691

456 FGAPILLARLIFYLERDAGAFTGGHDALKVTGFDSEPCSLSEKHTRPV--CAHT 511  
 334 IQKP-----SRTSPTATEENDYIM--INA3STNLVCSDVTDYHQPWQULLALYS 382  
 512 TVHRFLQRMP-----RGQATRQPICVFGTMNSQYSDCLPLGNAYAPLIRKPGD 561  
 383 DSPLILERKPKQLTETSSLSSRYKQVALPREDIFSTEADYR-ADPWFQEQKIVIQLNRT 441  
 562 QTEAAKATMDOTYRATERFLDQERL-----LDR-----GAPCSSEG 601  
 442 ATTLSLQIQFSTDAQALPRAEMRAERLKVTMILMMNNPKLERTVLGGTIALSOPGKG 501  
 602 ----LSSVIVDHPTR-----KILDTRARIEQTTOFMKL--VETRD----639  
 502 DFSPLWLLADGSKYRAPHYVSSEGRDILRKGQMSDFDAGLYHCSITNADADV 561  
 640 -YKIR-EGLSEATISMALTFDPYSGAF---CPITNFLVKRTHLAVVQDLSOCHV 691  
 562 LTYRITVVEPYGESEHTDSGVQHTVWVGETDLPCSTG-----VPDASIS--WI 608  
 692 FYGOVQEGRNFRNFQFVPLVRRFVDFLNGGFISTSITVTLSEGPYS--APNPT----743  
 609 LPGNTYFQSOPSSDR-----QIINNGTIRLQYT-PKDQGHYQCVANPSGADPSS 657  
 744 -----LGQDAPAGERTFDGDIAVRVEVITDIRVQNRVVFSGNCNTLSEBAPR 791  
 658 FKSVQKGQRMVHEBDRAGGGGLGE-PNSVSYLKOPLASLX---LSASALTSGEAGKQ- 711  
 792 LVGLASAYQRQBKRVDMLHGALG-FLIKQPHGLLPRGMPPNSKSBNPONFWTLQ--R 847  
 712 ----VSCVHRCKNKHDLJHRRGDSLTURFRE--HERQLPLSARIIDPQRVAALLERARK 765  
 848 NOMPADKLTHEIT-----IAVAKRFTTEYYAINFOINLPPCTIGELAQFYMMANLILK 900  
 766 NSVP----KKQENTTYKPVPLAVPLVLTDEEKDASGM--PP-----802  
 901 YCDHSQYLINTSITGARRDFFPSVLAHWTRKDVTISAADETQAKALLEKTENIDELW 960  
 803 -DEFWMLKTKASGVGPRSPTADSGPVNHFEMTISASGTEVSTVNPTQLO-SEHPDFK 859  
 961 TTAFTSTPHLVRAM-----NQRPVYLGISISKYTHGAAGNNRVRQAGHWSG-- 1001  
 860 LFSVTINGTAVTSMNPASKIEDTNQNIIIP-SVAEYRDSA-----QGRGSSQ 912  
 1007 --LNGGKVNCPLETFDRTRRFLIACPRGFFI--CPVTG--PSSGN 1045  
 913 AHPVTCGN---MATYGTINTYSSFTSKASTVYQPINPTESTYQPIKPTGVSRPSSD 966

RESULT 21  
 JS-10-454-351-13  
 Sequence 13, Application US/10454351  
 Publication No. US20040053301A1  
 GENERAL INFORMATION:  
 APPLICANT: Quark Biotech Inc.; Paz Binat, et al.  
 TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTION  
 FILE REFERENCE: 010/PCM2-2; USES THEREOF  
 CURRENT APPLICATION NUMBER: US/10/454-351  
 CURRENT FILING DATE: 2003-06-04  
 PRIORITY APPLICATION NUMBER: US/09/991,630  
 PRIORITY FILING DATE: 2001-11-06  
 PRIORITY APPLICATION NUMBER: US/09/905,129  
 PRIORITY FILING DATE: 2001-07-13  
 PRIORITY APPLICATION NUMBER: US/09/802,318  
 PRIORITY FILING DATE: 2001-03-08  
 PRIORITY APPLICATION NUMBER: US/09/729,485  
 PRIORITY FILING DATE: 2000-12-04  
 PRIORITY APPLICATION NUMBER: US/09/312,216  
 PRIORITY FILING DATE: 1999-05-14  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 13

LENGTH: 2597  
 TYPE: PRT  
 ORGANISM: *Rattus species*  
 FEATURE: misc\_feature  
 NAME/KEY: (1): (257)  
 LOCATION: OTHER INFORMATION: 'x' can be any amino acid  
 US-10-454-351-13

Query Match 1.9%; Score 120.5; DB 12; Length 2597;  
 Best Local Similarity 18.6%; Pred. No. 0; 67; Mismatches 287; Index 233; C

416 AGPHLAANPQTD---RDGHVLLSSQSTGSSNTE-----FSYDYL  
 274 SGALCTREPTIDPSLKSLSLVTDENGSSASTSPQDFIEPPFGSLSLNNTXXSGNKA

456 FGAPLARLILFYLERCDAGAFIGGHDALKYTGTFDSEIPLCSLEXHTRPV-----  
 334 IQKE-----SRTSPTAFTENDYIM---LNASEFTNLVSYDQVNHQIOPQWQL  
 512 TVHRLQRMP-----RFGQATROPIGVFTGTMNSQYSDCDPLGNYAPYLIL  
 383 DSPLILERKPQLETPSLSLSSRYKVALRPEDIFTSIAEDVR-ADPFWFQEQKIVL  
 562 QTEAAKATMQDTYTRATLERLRFIDLEQERL-----LDR-----GAP  
 442 ATTUSTLQIQFSIDQIAQIPRAEMRAEFLKWTMILLMMNPKLERTLVGGTIALS  
 602 -----LSSVYDHPTR-----RILDTRLARIE-OTTIQFMKV-----VETRD  
 502 DPSHLEWLADGSKVRAPYVSEDGRILIDKNGKLELMADSIDAGLYHCISTND  
 640 -YKRR--EGLSERATHSMALTEDPYSGAF---CPITNFVLRKTHLAVYQDLS  
 562 LTVRITVVEPYGSETHDSCVQHTVVTGTLDPCLSTS-----VPDASIS  
 692 FYGGOVEGRNFRNOQPYVLRERFVLDLNGGGFITSRINTVLSGPVS -APNPT-  
 609 LPGNTVFESQPSRDR-----QIUNQNGTLRILQVTF-PKDQGHYQCVAAFPG  
 744 -----LGQDAPAGRTPDGLARSVVEVIRL-----TRVQEVVFSGNCTNLSE  
 658 FKVSVQKQVQRMVEHDREGGSGIIGE -PNSSVS1KQPSLSK-----LSALSALTSE  
 792 LVGLASAYORQEKRVDMLHGALG -FLKOFQHGLFPRGMPPNSKSPNPFQWFWTL  
 712 ---VSGVHRKRNKRDLIHRRGDSTLRFRE -HRRQPLPSARRDFQRAALL  
 848 NQMPDADKLTHEIT-----IAAVKRFETEYAAINFNLNPPTCIGELAQFTWA  
 766 NSVP---RKQENTIVKPVPLAVPL-----DEEKAQSGN-----PP-----  
 Db 901 YCDHSQYLINTLTSITGARRPRDPSVILHWRKDVTSAADIEQAKALLEKTN  
 Db 803 --DEEFMVLTKTAKSCVPGISPTADGPVNHGFMTSIASTEVTPNPTLQ-SEH  
 Qy 961 TTAFFSTHLVRAAM-----NQPPMVVLGJISTSKYHGAGNNRVOQGN  
 Db 860 LFSVTTGATVKSNSPIASKIEDTNTQNPILIP-SVAEIRDSA-----QAGR  
 Qy 1007 ---LNGGKVNQVPLFDRTRFLACPRGF1-----CPVFG---PS  
 Db 913 AHPVFGN---MATVGHNTYSSSETSKASTVQPINPTESYGPQIPTGVSRPS

RESULT 22  
 US-09-729-485A-2  
 Sequence 2 Application US/09729485A  
 Publication No. US2009022226A1  
 GENERAL INFORMATION:  
 APPLICANT: Quark Biotech, Inc.  
 APPLICANT: Einat, Paz

APPLICANT: Segey, Orbit  
 APPLICANT: Skalitter, Ramii  
 APPLICANT: Feinstein, Alexander  
 APPLICANT: Faerman, Alexander  
 TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF  
 FILE REFERENCE: 540579-2007  
 CURRENT APPLICATION NUMBER: US/09/729,485A  
 CURRENT FILING DATE: 2000-12-04  
 PRIOR APPLICATION NUMBER: 09/729,485  
 PRIOR FILING DATE: 2000-12-04  
 PRIOR APPLICATION NUMBER: 09/632,862  
 PRIOR FILING DATE: 2000-08-04  
 PRIOR APPLICATION NUMBER: 60/207,821  
 PRIOR FILING DATE: 2000-05-10  
 PRIOR APPLICATION NUMBER: 60/084,944  
 PRIOR FILING DATE: 1998-05-11  
 PRIOR APPLICATION NUMBER: 60/085,673  
 PRIOR FILING DATE: 1998-05-15  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 2  
 LENGTH: 2597  
 TYPE: PRT  
 ORGANISM: Rattus species  
 FEATURE: NAME/KEY: MISC FEATURE  
 LOCATION: (1).(2597)  
 OTHER INFORMATION: "Xaa" can be any amino acid

US-09-729-485A-2

Query Match 1.9%; Score 120.5; DB 12; Length 2597;  
 Best Local Similarity 18.6%; Prod. No. 0.07;  
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;

Dy 416 AGPHLAANPQTD--RDGHVLLSSQTSGSNTT--FSDVYLAITCG 455  
 274 SGAFCLCTPTIDPSLKSLSLVIQEDNGSAASTSQDFIPPGSLSLNMTXXSGNKADIVCS 333  
 Dy 456 FGAPLLARLLFYLERCDAGAFTGCGHDALKYVTGTFDSEBIPCSLCEKHTRPV---CAHT 511  
 334 1QXP-----SRTSPTAFTBNDYIM-LNNSFSTNLVCSVDYNEHQVWQLLALYS 382  
 Dy 512 TVHRLRQMP-----REFQATROPIGFGTMNSQYSDCDPLGNYAPYLIRKPGD 561  
 383 D\$PILERKPOLTEPTPSLSSRYYCQVALRPEDITSIEADVR-ADPFWFQQEIKIVLQINRT 441  
 Dy 562 CTEAKATMQDQTYRATBLRFLDIEQERL-----LDR-----GAPCSSEG 601  
 442 ATTISTLQLQFESTQIAQIALPRAEMRAERLKWTMVLMNNPKLER TVLVGGTIALSCPSEG 501  
 Qy 602 -----LSSVTVDHPHTF-----RILDTLARIE-QTTQFQKVL---VEPRD----- 639  
 Ddb 502 DPSHLEWLIAADGGSKVRAPIVSEGRILLDKNGKLEMQMDSFAGLYHCISTNDADYV 561  
 Dy 640 -YKIR--EGLSEATHSMALTFDPSGAF---CPIITNFLVKTTHAYVQDLALSOCHCV 691  
 562 LTYRITVWPYGETHDSCGQHTVVTGETLDPPLSTG-----VPDASTS---WI 608  
 Qy 692 FYGGQVEGENFRNQFQPVLRFFYDLENGQFISTSRTVTLSEGPVS--APNP----- 743  
 Ddb 609 LPGNTVFSQPSRSD-----QILNNGTLLRQVTP-KDQGHYQCYAANPSGADFSS 677  
 Dy 744 -----LGODAPAGRTEFFDGLARVSVENTDIEVNRVVFSGNCTNLSEARAR 791  
 Ddb 658 FKVSVQKICQRMVBFHREAGGSGGE-ENSSVSKQPSLK---LSASALTGEAGKQ- 711  
 Qy 792 LVGLASAYORQEKRVDMLHAGL-FLLKQFHGLFPRGMPSNSSPNPWFILQL--R 847  
 Ddb 712 ---VSGVHRKRNQDLIHERRGQSTLRFRE-HRQDPLSARIDPWRVAILEKAKK 765  
 Qy 848 NQMPADKLTHEEITI-----IAVAKRTEEEVAAINFNLPPCIGELAQFYMANLTK 900

Qy 602 -----LSSVIVDHPPTFR-----RILDULRARIE-OTTTOFMKVLF---VETRD----- 639  
 Db 502 DPSPHDEWLILADGSKVRAPPVSEDRILLDKLGELOQNAQSDAGLYHCISTNDADADV 561  
 Qy 640 -YKIR- EGELESAHTSMALTEDPSGAF -- CPTINFLVKRTHLAVYDQDLSQCHCV 691  
 Db 562 LTYR-TVVEPYGESEHDSGVQHTVYVTGETLDPCLSTG-----VPDASIS---WI 608  
 Qy 692 PYQQVEGRNFRNQFOPVLFRRFVDFLNCGFISRSITVTLSECPVS - APNFT----- 743  
 Db 609 LGNTVFSQSRDR-----QILNNQTLRLIQT-PKDQSYHOCVAAANPSGADSS 657  
 Qy 744 -----LGODAPARTFEDDLARVSVEVTRDVRKRNRFVSGNCNTNSEAAR 791  
 Db 658 PKVSYQKGGQRMVERDREAGGSGLG-E-PNSSVSLKQPAKIK---LSASALTSEBAGQ- 711  
 Qy 848 NQMPADKLTHEEITT-----IAAVKRFEYEAIAINFNLPPTCIGELAQFYMANLILK 900  
 Db 792 LVGLASAYQOERKRYTDMHLHGAGL-FLLKQFHGLFPRGNFNSPSPNPWFILQ---R 847  
 Db 712 ---VSGVHREKNGHDLIARRGDSLTLRRE- -HRRQQLSARRIDPRAALLEZAKK 765  
 Qy 766 NSVP---KHOENTTYKPVPLAVPLVLTDEKDASGM-PP----- 802  
 Db 901 YCDHSQYLINTLTSITGARRPRDPSVLFMIRKDTSAADIEQAKALLEKTNPELW 960  
 Qy 803 -DEEFMVLKTKASGYPGRSPTADESGPVNGFMTSIASTGEVSTYNPOTIQ-SEHLPDFK 859  
 Qy 961 TTAFTSTHLYAAM-----NQRPNVVIGLISIISFHAGAAGRNVFOQAGNWSG -- 1006  
 Db 860 LFSVTINGTAVTKNSNPIASKIEDTNQNTTIIFF-SVAATRDSA-----QAGRASSQS 912  
 Qy 1007 --LNGGKVNCPFLFDTRTTRFIACPRGGFT-----CPVTCG- PSSGN 1045  
 Db 913 AHPVIGON---MATHGHTNIVYSSFTSKASTVLIQDINPTESYGPQIPITGVSRFSSSD 966  
 Qy 744 -----LGQDAPAGRFTEDGDLARVSYEVIRDIRKVRVVFSGNCNTNLSEARAR 791  
 Db 658 FKVSVQKGQRMVYEHDRDAGGSGLGE PNSSYSLKQASLK---LQASALTGSEAGKQ- 711  
 Qy 792 LVGLASAYQOERVDMHAGL-FLKQFHGLFPRGMPPNKSNSPNQWENTLLO---R 847  
 Db 712 ---VSGVHREKNGHDLIARRGDSLTLRRE- -HRRQQLSARRIDPRAALLEZAKK 765  
 Qy 848 NQMPADKLTHEEITT-----IAAVKRFEYEAIAINFNLPPTCIGELAQFYMANLILK 900  
 Db 766 NSVP -- KKOENTTYKPVPLVLTDEKDASGM- -PP----- 802  
 Qy 901 YCDHSQYLINTLTSITGARRPRDPSVYLHWIRKDVTSAADIEQAKALLEKTNPELW 960  
 Qy 961 TTAFTSTHLYAAM-----NQRPNVVIGLISIISFHAGAAGRNVFOQAGNWSG -- 1006  
 Db 860 LFSVTINGTAVTKNSNPIASKIEDTNQNTTIIFF-SVAATRDSA-----QAGRASSQS 912  
 Qy 1007 --LNGGKVNCPFLFDTRTTRFIACPRGGFT-----CPVTCG- PSSGN 1045  
 Db 913 AHPVIGON---MATHGHTNIVYSSFTSKASTVLIQDINPTESYGPQIPITGVSRFSSSD 966

RESULT 24  
 US-09-729-485A-13  
 Sequence 13, Application US/09729485A  
 Publication No. US20020022056A1  
 GENERAL INFORMATION:  
 APPLICANT: Quark Biotech, Inc.  
 Binat, Paz  
 Segev, Orbit  
 Skaliter, Rami  
 APPLICANT: Feinstein, Elana  
 APPLICANT: Faerman, Alexander  
 GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF  
 TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF  
 FILE REFERENCE: 540579-2007  
 CURRENT APPLICATION NUMBER: US/05/729,485A  
 CURRENT FILING DATE: 2000-12-04  
 PRIOR APPLICATION NUMBER: 09/729,485  
 PRIOR FILING DATE: 1998-05-11  
 PRIOR APPLICATION NUMBER: 09/632,862  
 PRIOR FILING DATE: 2000-08-04  
 PRIOR APPLICATION NUMBER: 60/1207,821  
 PRIOR FILING DATE: 2000-05-10  
 PRIOR APPLICATION NUMBER: 60/084,944  
 PRIOR FILING DATE: 1998-05-11  
 PRIOR APPLICATION NUMBER: 60/085,673  
 PRIOR FILING DATE: 1998-05-15  
 NUMBER OF SEQ ID NOS: 22  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 13  
 LENGTH: 597  
 TYPE: PRT  
 ORGANISM: Rattus species  
 FEATURE: MISC FEATURE  
 NAME/KEY: (1)\_(2597)  
 LOCATION: (1)\_(2597)  
 OTHER INFORMATION: "Xaa" can be any amino acid

RESULT 25  
 US-09-802-318-2  
 Sequence 2, Application US/09802318  
 Publication No. US20020086825A1  
 GENERAL INFORMATION:  
 APPLICANT: Einat, et al.  
 TITLE OF INVENTION: AND USES THEREOF  
 FILE REFERENCE: 540579-2007-1  
 CURRENT APPLICATION NUMBER: US/09/802,318  
 CURRENT FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: 09/632,862  
 PRIOR FILING DATE: 2000-08-04  
 PRIOR APPLICATION NUMBER: 60/1207,821  
 RESULT 26  
 US-09-802-318-2  
 Sequence 2, Application US/09802318  
 Publication No. US20020086825A1  
 GENERAL INFORMATION:  
 APPLICANT: Einat, et al.  
 TITLE OF INVENTION: AND USES THEREOF  
 FILE REFERENCE: 540579-2007-1  
 CURRENT APPLICATION NUMBER: US/09/802,318  
 CURRENT FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: 09/632,862  
 PRIOR FILING DATE: 2000-08-04  
 PRIOR APPLICATION NUMBER: 60/1207,821

PRIOR FILING DATE: 2000-05-30  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 2  
 LENGTH: 2597  
 TYPE: PRT  
 ORGANISM: *rattus* species  
 FEATURE: misc\_feature  
 LOCATION: (1)..(2597)  
 OTHER INFORMATION: 'x' can be any amino acid  
 US-09-802-318-2

Query Match Score 120.5; DB 12; Length 2597;  
 Best Local Similarity 18.6%; Pred. No. 0.67;  
 Matches 145; Conservative 113; Mismatches 287; Indels 233; Gaps 40;  
 LENGTH: 2597

QY 416 AGPHDAAANPQTD--RDGHVLTSSOSTGSNSTE-----FSVDVIALICG 455  
 Db 274 SGAFLCTKPTIDPSLKSLSLTQEDNGSASTSPQDPFIEPGFSS1PCSLCEKHTFV---CAHT 511  
 QY 455 FGAPLLARLLFYLERCDAGAFTGGHDALKYVTGFDSE1PCSLCEKHTFV---CAHT 511  
 Db 334 IOKP-----SRTSPATATEENDYIM--LNASSTP1VCSDVNH1QPVWQLLALYS 382  
 QY 334 IOKP-----SRTSPATATEENDYIM--LNASSTP1VCSDVNH1QPVWQLLALYS 382  
 Db 334 IOKP-----SRTSPATATEENDYIM--LNASSTP1VCSDVNH1QPVWQLLALYS 382  
 QY 416 AGPHDAAANPQTD--RDGHVLTSSOSTGSNSTE-----FSVDVIALICG 455  
 Db 274 SGAFLCTKPTIDPSLKSLSLTQEDNGSASTSPQDPFIEPGFSS1PCSLCEKHTFV---CAHT 511  
 QY 456 FGAPLLARLLFYLERCDAGAFTGGHDALKYVTGFDSE1PCSLCEKHTFV---CAHT 511  
 Db 334 IOKP-----SRTSPATATEENDYIM--LNASSTP1VCSDVNH1QPVWQLLALYS 382  
 Db 512 TVHLRQMRP-----EFGQATRQPIQIGFGTNSQYKSDCDPONYAPYL1RKPGD 561  
 QY 512 TVHLRQMRP-----EFGQATRQPIQIGFGTNSQYKSDCDPONYAPYL1RKPGD 561  
 Db 383 DSPLLERKPKQIETPSLSSRYKQVALRPEDEFTS1EADYR ADPFMFOQEKIVLQLNRT 441  
 QY 562 QTEAAKATMDQTYRATLERLPTIDEBRL-----LDR-----GAPCSSEG 601  
 Db 562 QTEAAKATMDQTYRATLERLPTIDEBRL-----LDR-----GAPCSSEG 601  
 QY 602 ---LSSVTDHPTF-----RILDTHRAR1-QTTQFEMKYL---VETRD---- 639  
 Db 602 ---LSSVTDHPTF-----RILDTHRAR1-QTTQFEMKYL---VETRD---- 639  
 Db 640 --YKIR--EGLSEATHSMALTFDPSGAF---CPTINFLYVKRTHLAVYDODLSSQCHV 691  
 QY 640 --YKIR--EGLSEATHSMALTFDPSGAF---CPTINFLYVKRTHLAVYDODLSSQCHV 691  
 Db 562 LTYRITVVEPYGESTDIDSGVQHTWVGETLDPCLSTG-----VPPASIS---WI 608  
 QY 562 LTYRITVVEPYGESTDIDSGVQHTWVGETLDPCLSTG-----VPPASIS---WI 608  
 Db 692 FYGQQVEGRNFRNQOFQVFLRRFVDLNGGP1STRS1TIVLSEGPPS---APNPT---- 743  
 QY 692 FYGQQVEGRNFRNQOFQVFLRRFVDLNGGP1STRS1TIVLSEGPPS---APNPT---- 743  
 Db 609 LPGNTVFSOPRDR-----Q1LNGT1R1LQY---PKDQGHYQCVANPSCADESS 657  
 QY 609 LPGNTVFSOPRDR-----Q1LNGT1R1LQY---PKDQGHYQCVANPSCADESS 657  
 Db 744 -----LGQDAPAGRTFDGDLARYVEVERD1R1VKNR1VVFSGNTNLSEARAR 791  
 QY 744 -----LGQDAPAGRTFDGDLARYVEVERD1R1VKNR1VVFSGNTNLSEARAR 791  
 Db 658 FKVSQKQKQMRVHEDRAGSSGLGE PNSVSYSLQPKASLK---LSASALTGSBAGK- 711  
 QY 658 FKVSQKQKQMRVHEDRAGSSGLGE PNSVSYSLQPKASLK---LSASALTGSBAGK- 711  
 Db 792 LVGLASAYQREKVRDMLHGALG-FUJKQFHGLLFRGMPNNKSPNQWENFLQ--R 847  
 QY 792 LVGLASAYQREKVRDMLHGALG-FUJKQFHGLLFRGMPNNKSPNQWENFLQ--R 847  
 Db 712 ---VSGVHRKRNKHDL1HRRQGDS1URFRE--HERQPLIUSARRDQPVIAALLEKAKK 765  
 QY 712 ---VSGVHRKRNKHDL1HRRQGDS1URFRE--HERQPLIUSARRDQPVIAALLEKAKK 765  
 Db 848 NQMPADKLTHEBTT-----IAAVKRFETREYAA1NFN1NUPPTC1GELAQFYMANL1K 900  
 QY 848 NQMPADKLTHEBTT-----IAAVKRFETREYAA1NFN1NUPPTC1GELAQFYMANL1K 900  
 Db 766 NSVP-----KKQDENTTYKPVPLAVPLVYD1K2DASCM1--PP----- 802  
 QY 766 NSVP-----KKQDENTTYKPVPLAVPLVYD1K2DASCM1--PP----- 802  
 Db 901 YCDHSQYLN1NTLTS1T1GARRPRDPSY1LHWIKRDVTSAA1ETQAKALLEKTN1PELW 960  
 QY 901 YCDHSQYLN1NTLTS1T1GARRPRDPSY1LHWIKRDVTSAA1ETQAKALLEKTN1PELW 960  
 Db 803 --DEEFMVLKTKASGPGRSPPTADSGPVNNGMFTS1ASGTEVSTYNPQTLQ-SEHLPDFK 859  
 QY 803 --DEEFMVLKTKASGPGRSPPTADSGPVNNGMFTS1ASGTEVSTYNPQTLQ-SEHLPDFK 859  
 Db 961 TTAFT1STH1VRAAM-----NQRMVWLG1S1SKYHGAGN1RVEQAGNWSG-- 1006  
 QY 961 TTAFT1STH1VRAAM-----NQRMVWLG1S1SKYHGAGN1RVEQAGNWSG-- 1006  
 Db 860 LPSVTINGTAVTKSMNPSIASKIEDTNQNP1IIP-SVAEIRDSA----QAGRASSQ 912  
 QY 860 LPSVTINGTAVTKSMNPSIASKIEDTNQNP1IIP-SVAEIRDSA----QAGRASSQ 912  
 Db 1007 ---LNGCKNVCPLFTDFTRRFL1ACPRGGF1-----CPVTG--PSSGN 1045  
 QY 1007 ---LNGCKNVCPLFTDFTRRFL1ACPRGGF1-----CPVTG--PSSGN 1045  
 Db 913 AHPVTGSGN----MATIGHNTYSSFTS1ASTVQ1NPNTESYGPQ1P1TGVS1PSSSD 966  
 QY 913 AHPVTGSGN----MATIGHNTYSSFTS1ASTVQ1NPNTESYGPQ1P1TGVS1PSSSD 966  
 Db 903 --DEEFMVLKTKASGPGRSPPTADSGPVNNGMFTS1ASGTEVSTYNPQTLQ-SEHLPDFK 859  
 QY 903 --DEEFMVLKTKASGPGRSPPTADSGPVNNGMFTS1ASGTEVSTYNPQTLQ-SEHLPDFK 859  
 Db 961 TTAFT1STH1VRAAM-----NQRMVWLG1S1SKYHGAGN1RVEQAGNWSG-- 1006  
 QY 961 TTAFT1STH1VRAAM-----NQRMVWLG1S1SKYHGAGN1RVEQAGNWSG-- 1006

RESULT 27

/ Sequence 13: Application US/09802318

/ GENERAL INFORMATION:

/ APPLICANT: Binat, et al

/ TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THEREOF

/ FILE REFERENCE: 5405/9-2007.1

/ CURRENT FILING DATE: 2001-03-08

/ PRIOR APPLICATION NUMBER: 09/624,862

/ PRIOR FILING DATE: 2000-08-04

/ PRIOR APPLICATION NUMBER: 60/207,821

/ PRIOR FILING DATE: 2000-05-30

/ NUMBER OF SEQ ID NOS: 25

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO: 13

/ LENGTH: 2,997

/ TYPE: PT

/ ORGANISM: Rattus sp

/ FEATURE: misc feature

/ LOCATION: (1) ..(2597)

/ OTHER INFORMATION: 'x' can be any amino acid

us-09-802-318-13

Query Match 1.9%; Score 120.5; DB 12; Length 2597;

Best Local Similarity 18.6%; Pred. No. 0.67; Indels 233; Gaps 40;

Matches 145; Conservative 113; Mismatches 287;

Query 416 AGPHIAANPDTD--RDGHTLSSQSTGSSNTE-----FSDYALICG 455

Db 274 SGAFIILCTKPIDPSIKSKRFLYLERCDAGFTGGDAKLYVGTQDNGSSTSPODFIEBFGSLSLNMTXXSGNKADYMS 333

Query 456 FGAPLLARLFLYLERCDAGFTGGDAKLYVGTQDNGSSTSPODFIEBFGSLSLNMTXXSGNKADYMS 333

Db 334 IQKP-----SPTSP1PTEENDYM--LNAFSFTNLVCSVDYNEIQPTWQLLAYS 382

Query 512 TVHRLRQMP-----RGQATQDPIGVFTMNQSYSDCPLGNYAPYLIRKEGD 561

Db 383 DSPLLERKEPQLTETPSLSSRYKQALRPEDIFTSIDEAVR-ADPFWFQQEKIVLQNRT 441

Query 562 QTEAKAKMDDTYRATLERLIFDLEQERL-----LDR-----GAPCSSEG 601

Db 442 ATTSTLQDSTQDQIAFLRAENRAERLQKWTMILMNNPKLERTVLYGGTIALSCPKG 501

Query 602 -----LSSVIVDHPTR-----RILDILRARIE-QTTQEMKVL---VETRD---- 639

Db 502 DPSPLERWLLADGSKVRAPIVSEDRILLDKNGKLELQMDAESPAGLYHCISNDADAV 561

Query 640 --YKIR--EGLSEATHSMALTFDPSGAF---CPITNFLVRETHLAYQDIALSOQCHCV 691

Db 562 LTYRTVVEYQGESTHDSGVQHTVVTGETLIDLPLSTG----VPDASIS---WI 608

Query 692 FYGQQVEGRNQFRNQFQPVLRREEFVDFLNGGFIISTRSTIVTLSSEGPSV--ANPT---- 743

Db 609 LPGNTVFSQPSRDR-----QILNNGTLLRQVTFKDQGSHYQCVANPSGADFSS 657

Query 744 -----LGODAPAGRTFEGDGLARVSVEVTDIIRVKRNVVFSGNCNTNSEAAR 791

Db 658 FKVSVQKKGQRMVHEDREAGSGLGE--PNNSVSLKQPSLAK---LSASALTGEAQRQ- 711

Query 792 LVGLASAYQFQEKRVDMLHAGL-FLIKOFPHGLLPRGNPNSPKSPNPKQWFTWLLQ--R 847

Db 712 -----VSSVHVKHDKLHRRGDSTLRRPRE--HRRQPLSARRIDQQRWAALLEKARR 765

Query 848 NQMPADKLTHEITT-----IAAVKRTEBEYAAINFINLPTCTGELAQFYMANLILK 900

Db 766 NSVP----KKGENTTYKPVPLAVPLTDEKDAGSMI--PP----- 802

Query 801 YCDHSQQLINTLTSITGARRPRDPSSVLEMRKDVTYSAADIEQAKALLEKTENLPELN 960

Db 803 --DEEFMVLKTKASGIVGRSPTAQSSPVNNGEMTSASGTEVSTNPQTLO--SEHLPDFK 859

Query 961 TIAFTSHVLAAM-----NQRPNVVLGISISKYHGAAGNVRQAGHWSG- 1006

Db 860 LFSVTINGTAVTKMSKNSIASKIEDTQNQNPILIFP-SVAETRDSA----QAGRASSQS 912

Query 1007 ---LNGCKNVCPBLFTPDRTRFLIACRGFTI-----CPVITG--PSSGN 1045

Db 913 AHPVTGGN---MATYGHNTYSSFTSKASTVLLQPINPTESYGPQIPTGYSRPSSSD 966

RESULT 28

US-10-329-079-11

; Sequence 11, Application US/10329079

; Publication No. US2003198981A1

; GENERAL INFORMATION:

; APPLICANT: FARNET, Chris

; APPLICANT: ZAZOPOULOS, Emmanuel

; APPLICANT: STAFFA, Alfredo

; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES

; FILE REFERENCE: 3.002-11US

; CURRENT APPLICATION NUMBER: US/10/329,079

; CURRENT FILING DATE: 2002-12-24

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 11

; LENGTH: 5245

; TYPE: PT

; ORGANISM: Streptomyces fradiae

US-10-329-079-11

Query Match 1.9%; Score 120; DB 14; Length 5245;

Best Local Similarity 20.2%; Pred. No. 2.6; Mismatches 434; Indels 464; Gaps 68;

Matches 262; Conservative 138; N mismatches 434; Indels 464; Gaps 68;

Query 102 PSSAAPVULTRACNAARERFGFSRCQGP-----VDGAVETTGAECITRL-----GL 147

Db 464 PAAAEPADEAGLEAVCQDFTARQQAATPEAPAVVGGEPAVTFQEAADAVSRLARLLISRGA 523

Query 148 EPENTILLYVTTALFKEAVFMNVFLHYGGGLDIVHNGDVIRPLFVQLFMPDVNRLV 207

Db 524 GP-----VRYVACLDENALWTTV-----LAVLRSGAHVPL----- 556

Query 208 PDPENTHRSIGECPVYPTPYNTGLCHLHDCTVIAPIAVALRVENVTAVARGAAHIAF- 266

Db 557 -DPRSPER-----LAVERD--VAPPLVLAERATEAAVADLAAFPFLV 597

Query 267 -DENHEAV-----LPPDTTYYTQFQSSSS-----TTTARG----A 297

Db 598 DDPSTERAIDALDGPVTDADRTAPLPGHAAVYVHTSGSTGRPKGVTVDHRLGSRLQ 657

Query 298 RNDVNNTSKPSPSG-GFERLASI-----MAADTAHLA----- 330

Db 658 HRRVTSRIRSAAGGQRAHVSSEPSDASWDPLLAVGHELMIDDLRFDPPGVAY 717

Query 331 -----EVIFTGIVEE----TPT----DIKEWPMFIGNEGTLPRLNAL 365

Db 718 FDRRIDYVDLTPTYPRSLLDGELFQGPPSLVALGGEMDGEILWLRRAARVTAM 777

Query 366 GSY-----TARYA-----GVIGAMVFSPSNALSXTEVEDSGNTAEKDGGGPFSN 411

Db 778 NTYGPTRTAVDWTYLGDLPGTGRPV--PRWAY--VLDAGLRPVPGVLGELY-- 830

Query 412 FYQFAGBHLAANPOTDRDGHVLSQSTGSNTFSDYDYLALICGFCA-----LLAR 463

831 --LAGPGVARYLQG--HALTAER--FVACPEGKPGEMYRTCDLAR 871  
 465 L----LFLYLERCD----AGAF----TGCHGDAALKY 487  
 872 WLPDGHLYVGRGDEQVKIRGPRIEGVEAAIRLEGGVAAAVTRDPTTRLGYV 931  
 488 TGTFDSEFCISLCEKHTRPVCAHTTVERQMP----RFGQATRQPIGYGFTMSQ 541  
 QY ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  
 Db 932 VGPBDAD----DARLPA----EVLAIRDRDLPDHLVPSAIVRLRPLVNTSGKLDRA- 981  
 QY 542 SDCDPLGNYAPYLRLRKGDQTEAKATQMDTYRATERLFDLEQRLLRGAPCSSEG 601  
 Db 982 -ALPAZPDADEPAGRPP----RATALEEVCAFLAEVL----G 1014  
 QY 602 LSSVIVDHTFTRILLDTLARIEEQTTOMKVLIVETDYKIREGLSPATHESMALTDPYS 661  
 Db 1015 AGSYGIDDDFFGRGDSLIS----IQLVGSAR - RAGL----TFTYTRQVEFLR 1058  
 QY 662 GAFCPITNFVLRKTHLAVVQDIALSQCCHCFCYQQVEGRNFRNQFQEVLRFDLFGGG 721  
 Db 1059 PAALAA----ARRTDAAGEDDPLA----VGP----LPLPVVAAETLAAAGG 1098  
 QY 722 FLSRSITVLSGCPVSAAPNPTLGODAPAGRITFDGLARVSVEV----IRDIVYKNR- 774  
 Db 1099 PVHSYNQSVVLAQSPDAAFPDDV -RDALQALUDRHDALRVAAPGPRGWLDRYBEAG 1156  
 QY 775 VVFSGNC----TNLs -EAARLVLCLASAYQREKRVDMHLHAGLFLKQFHGLLFp 826  
 Db 1157 TVAACERCLRIRIDATGMSDELLAAQAABATA ---RACLDPLAGAL----VSAWVFD 1206  
 QY 827 RGMPP----NSKSPNPKW----FVTLORNQMPADKLTHEITTIAAVKR 869  
 Db 1207 RGDPRGRLVTVHLAVLAVGWSVRLGGLREKARLRRGRRBPLPRTGTSURTWAT--RL 1264  
 QY 870 TEEYAAATINFNLNPPTCIGBLAQFYMANLILCYCDHSOYLINTLTSITGTAIRPRD -PSS- 927  
 Db 1265 TERAT----DPAVTAQL-DHWTATLADGPAPGSPRLDRTRDVTAVSISGELPASL 1316  
 QY 928 -----VLIHWI-RKDVTSAADIETOAKALLEKTENL-- 956  
 Db 1317 TTDILGPAAFAFGVNDLILTTAFALAIVAHWGEEDAPVLDLRESHG----RTEBLVPG 1371  
 QY 957 PELWTTA -FTSPHLVRAAMNQRPVMVLLGISISKYHGAAGN----NRVFOQNWNSGLNG 1009  
 Db 1372 ADLSRTVGMFTSVPVRLAAGR ---VTAADIAERAPAVGDAIKRKEQRLAVPDGLGH 1427  
 QY 1010 G--KVNVCp----LFPFDYRTRFIACTPREGFICPV -TGPSSGNRETTLSQD 1053  
 Db 1428 GLLRHLNPDTAPRURGLARARFSEFNYLGRFAAEQGASEDSWNLGSGPAGQHPTDPLDHE 1487  
 Qy 1054 VRGLIVS----GAMVOLAIATVVAZGARQHMAFDWLSLTDDEFLARDLZLHDQ 1108  
 Db 1488 IEVNVTAAEGDPGRLTRWYTAGL----LTEEE---- 1518  
 Qy 1109 IICLETPTVVEGAEAVKILDEKTTAG-DGETPTNL 1145  
 Db 1519 -VRLTRSL -ALHAY -VGHATAEGAGGLSPSDVA 1551

RESULT 29  
 US-10-425-114-71520  
 ; Sequence 71520, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT Liu, Jingdong  
 ; APPLICANT Zhou, Yihua  
 ; APPLICANT Kovalic, Steven E  
 ; APPLICANT Tabaska, Jack E  
 ; APPLICANT Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313) B

; CURRENT APPLICATION NUMBER: US/10/425, 114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO: 73120  
 ; LENGTH: 452  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: UC-ZMFLB732270E12\_FLI.pep  
 US-10-425-114-71520  
 Query Match 1.9%; Score 118; DB 12; Length 452;  
 Best Local Similarity 22.7%; Pred. No. 0.052;  
 Matches 91; Conservative 36; Mismatches 132; Indels 142; Gaps 22;  
 Qy 195 FVQLEMPDVNRLVPDPFNTHRSIGEGFVYPTPYNTGCLHLHDCTAPMAVALRTRV 254  
 Db 90 FVQRMRPVSTEAVPQ----HH----ODDIETS -NGSSKKIEDCI---- 126  
 Qy 255 TAVARGAAHAFDENHEGAVLPPDITYTYFQSSSSGTTARGARRNDNTSTSKEPSGSG - 312  
 Db 127 -----ASSEN-----LPPD-----GTTNVEVTDASSKONLSFGYS 160  
 Qy 313 -----GFERRLA-----SIMADT-----SIMP-----G 336  
 Db 161 STKVVIEDAELSGNKDAGSNYFGTHESSVEAQSRDLYHFSIPLFLHDFYRNL 220  
 Qy 337 GIEBETPTD1KEWMFPIGMEGLPRLNALGSGTARVAGVIGANVFSNSALYLTEDSG 396  
 Db 221 NYFOSS-----ILGBENS----NKDGSQs---EGSGENDY---- 252  
 Qy 397 MTEADGGPPSFNFYQ --FASP----HLAA----NPQTDRGHFLSSST----G 439  
 Db 253 QAERAGMAGKSQSDFGIDKSKIPKPTFPLVMLKLNKNERIDKASDVLQSYSTOYNEA 312  
 Qy 440 SSNTFSVYDVTALICFGAPLARLFLYJERCDAGATFGHGDALKYTTGTFDSEIPCSL 499  
 Db 313 LENFTSISQRLGHTCMKGPAKRUV -YIPVIEVS -EGRLAHACKVTDFAF--IKAGL 367  
 Qy 500 C-EKHTRPACTAHTYHRLRORMPREGQAT---RQPIGYFG 535  
 Db 368 VFERDVERLKHATMVNRHRSRNKRNTWTDSDARGIFG 408

RESULT 30  
 US-10-084-846A-8  
 ; Sequence 8, Application US/100084846A  
 ; Publication No. US20040006626A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEITNER, GABRIELE  
 ; APPLICANT: MOHLWEG, AGNES  
 ; APPLICANT: TREZER, AXEL  
 ; APPLICANT: BECHTHOLD, ANDREAS  
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
 ; FILE REFERENCE: 1974-005  
 ; CURRENT APPLICATION NUMBER: US/10/084, 846A  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815  
 ; PRIOR FILING DATE: 2003-02-25  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO: 8  
 ; LENGTH: 19608  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces viridochromogenes  
 ; FEATURE:  
 ; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.  
 ; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.  
 US-10-084-846A-8

Query Match 1.9%; Score 118; DB 15; Length 19608;

Best Local Similarity 19.7%; Pred. No. 44;	Db	12590	CYQDAWPSAVGCSYVR-- SVRSTMSLAVGFSFORMLAGIS-----RERRF-----12631
Matches 240; Conservative 133; Mismatches 443; Indels 404; Gaps 62;	Qy	1033	GFICPVTTGPSSGNRETTLSDOVRGTVTSGAMVOLAIYATVRAYGARAQHMAFDWLSSL 1092
106 APNUTRACNAAREFGFSRQ---QGPVPGAVETTGAE----ICTRIGLEP-----149	Db	12332	-----SSRRRTTIVTESSPCSTSG-----RRTCAVAGSRSICAI-----CSR 12670
11736 APHSRPTRGARPGRHARCRGRGPPIGA---RGAPPPHASRSLRSPDSAPSNL 11792	Qy	1093	TDEELARDLIELHOOIQTLETPTVTEGCALEAVKILLEKITAAGGETPTNLAFNFDSC 11152
150 --ENTILYVLTALFKEAVEMCNVFLHYGLDIVH--INFGD----VIRILFPP 195	Db	12671	TSSS-----TRERSGGD-----R 12664
11793 ENLENNAKQFIRSAKGKPA-----GGLSPSHGCCRQSHAVQRALVQRLPPV 11842	Qy	1153	PSHDITTSVNLNISGSNISGS 1172
196 VOLMPD-----VNRLVDPDFNTHERSIGEGFVY-PPTFYNT 231	Db	12385	PANDITTSASAPPGSSVSGA 12704
11843 V-LGVPARHGGEALLERHTCVAEAGAQAQVAPVV----SLPVGTYLDPPVAGAQ 11895	Db	12385	PANDITTSASAPPGSSVSGA 12704
232 GLCLJHDCTVIAPAVALVRNNTAVARGAHLAEDENHE----GAVLIP-PDITYTYFQ 285	Qy	1031	RESULT 31
11896 GVOOQLRQFQIGQLG---BARDVYDLPRL---QPAFGDQDAPVHGVHPPVDDAATPVO 11949	Db	10-231-956A-325	; Sequence 325, Application US/10231956A
286 SSSGGTTARGARRNDVNSTSKPSGGFERRLAS-IMAADTALHAEVFTGIVYEETP 343	Qy		; GENERAL INFORMATION:
11950 RDAYAQVQPGEBQNDL-----LRELJGPVVAAPRAHRO-----	Db		; APPLICANT: Llorens, James B.
344 TDIXEWPMPFIMGEGLTPRINA-LGYYTARAVAG-----VIGANVFSNPA 386	Qy		; APPLICANT: Xu, Weiduan
11986 -----PMGGAVV-GEGDAYAARLGRVGRVGGDERRVLPGGARLDAAVLGVGLHDFGRA 12038	Db		; APPLICANT: Bogenberger, Jakob
387 --LYTLEVDS--GMTEAKDGGFPGPSFMRFYQ----FAGFHLAANPQTDRDGHYL 434	Qy		; APPLICANT: Holland, Sacha
12039 GLQAHJHECJDALHGTYYERRVGRVGGDERRVLPGRVGDHQVAGDHLGQPGI-ADVAVHE 12097	Db		; APPLICANT: Rigel Pharmaceuticals, Incorporated
435 SQSTGSSNTFSVDYALICGFGAPLLAFYLERCDAGAFTCGHGDALKYTG----489	Qy		; TITLE OF INVENTION: Modulators of Angiogenesis
12098 GVPAGDRLQTRQVPGVQLYQHGHPRRIAV-----PDAFAHVLGADPAR 12141	Db		; FILE REFERENCE: 021044-004100US
490 -TDFSEIPCPSCILCEKETRVPVCAHTYFHRLRMPREGQATRQPGVFTMNSQYSDCDPLG 548	Qy		; CURRENT APPLICATION NUMBER: US/10/231,956A
12142 STDDQDVPSSE--RTRAASVHVPYSLRIRVRPLRRLPPTW-RLWSPSTSRCAYDV	Db		; NUMBER OF SEQ ID NOS: 522
549 NYAPYLIRKPFQDQEAAKATMDQYTRERLFLDQEORLRL---RGAPCSSEGSS 604	Qy		; SOFTWARE: FastSBQ for Windows Version 3.0
12198 RGAATFTSVSRPITESSTRAPSIEAPRSIE-YNISLCATRQLPSMEVKGPRSCCTVSG 12256	Db		; SEQ ID NO: 325
605 VIVDHPTRFR----ILDTR--ARIEQTTOFMKVLYETRDYKIREGSEATHMSA-- 654	Qy		; LENGTH: 1479
12257 PMTAGPTMRREPEIFAPASTTRPTSSLASSSTSPTSMRV--SRDSSRCRPIRSVTLATS 12313	Db		; TYPE: PR
655 -----LTFDPPSGAFOPITNLVKTRLAVQDLSOCCHVFGQOEGRNFRNQ----705	Qy		; ORGANISM: Homo sapiens
12314 FQYRSITVPEPS--CP-----WSASC--RASVSSFFQDGMP 12349	Db		; US-10-231-956A-325
706 -----FQPVLRPRTFVLDLNGGPFISTRSITVTLSEGPVSAPNPTL-GDODAPGRT 753	Qy		Query Match Score 1.88; Best Local Similarity 18.5%; Pred. No. 0.97; Length 1479;
12350 ATASCTAELKAYPTLARSI--LGSWGP-STTAVTRPFS---SSATPNLRGSAATRANT 12403	Db		Best Local Similarity 18.5%; Pred. No. 0.97; Length 1479;
754 FDGDLLR---VSVEVTRDIRYKVRVVFSGCNCTNISBEAARLVLGASAYQKERRQVDMILH 810	Qy		Mismatches 118; Conservative 204; Indels 341; Gaps 47;
12404 CAAGLSSRKSATKSMPSITSPRM---TKSSSPRSRDTSTASASPR-----12449	Db		Matches 204; Conservative 211; Indels 341; Gaps 47;
811 GALGFLIKOFGLLPRGMPPNSKSNPONFW-----TLLQRNQMPADKL--THEEIT 861	Qy		162 FKEBAFVMCNVFLHYGGDIVHTNHGDVTRIPFLPFVMPD--VNRUAVDPDPTNTHRSIG 219
12450 GASCHWNTS-----RPNs-ADSPTAWISAVAPTTIPSDIPASLMEESTRTV 12498	Db		130 FKGLASLQEQLYHFNQET--LDPDSFQHLPKLE-RFLPHNMRITHVPGTFN-HLESMK 185
862 TIAAVKRFTEEYAAI--NFINLPPCTIGELAQFTMANLILKYCDHSQYINTLTSITGA 919	Qy		220 EGFVYPTPFYNTGLCHLHDCVYATPMAVLRVRNNTAVARGAHLAFLDENHEGAVLPD 279
12499 LIATGTSCLAEVGCRSLBPPPT-----NMSAFISHTLRS---12536	Db		186 RLRLDS---NRLHCC---DCEBILWADLLKTYAESSNAQAACIEYPRR-----227
920 RRPRDPBSVHLWIRKDVTSADIEQAKALLETKENLPELWTTAATSTHIVRAAMNORM 979	Qy		280 TYTYQSSSSGCTTARGARRNDVNSTSKEPSGGFERRLASTMAATPAHEVIENTGIV 339
12537 -----PSDQV--VSREIQMAGNSVQAORSTMRVFOVPPRPGRLARPHEPAVPCHELRSQ 10589	Db		228 ---IGRSVATTPELNCERPRITEPQ-----TIPRINAL-----GSYTPARVAGVIG 377
980 VV-----LGISISKRYHAGLGNRNVQAGMWSGLNGKRNVCPLFDRTRRIACPRG 1032	Qy		340 EERPTDKEWPMDIGMFG-----TIPRINAL-----GSYTPARVAGVIG 377
	Db		265 FTCAEAGNPKPETIIMNNELSMKTUSRLNLDGTLIMQNTQETQIYOCMARNVAG 324
	Qy		378 AMVFSPIANSALYLTVEPSGMTBAKDGDPGPSENFRPQFAGPHLAANQFTDR---DGHVIL 433
	Db		325 -----EVKQEVTLRYFGSP-----ARPTFVIQQNTEVLYGEVNTL 361
	Qy		434 SSQSTG-----SSNTERFVDYLALICSGFAPPLARLFLYLERCDAGAFTGGGGDA 483
	Db		362 ECPATGHPPPRISWTRGDRTPLEPVDPRVNNTPSGG-----LYIQ--NVVQGDSEY 410
	Qy		484 LKVTGTFDSEIFCSLCEKHTRPVCAHTVHLRORMPRFGQATROPIGVFG-TWNSQYS 542
	Db		411 ACBTANNDIS-----VATAFTIVQAPQFVTPQDBEVIEQTVDFD--453
	Qy		543 DCDPLGNVAPYLILRKEDQTEAKATMODYTRATERLRLFIDLEQERLLDRGA-PCSSSEG 601
	Db		454 -CEAKGNPPVIAWKGQSOLSY-----DREHVLSSGTLRISGVALHDQGQECOAVN 506

us-09-769-699-2.rapb

---

ORGANISM: Homo sapiens

US-10-211-462-87

Query Match 1.8%; Score 114.5; DB 12; Length 1496;

Best Local Similarity 18.5%; Pred. No. 0.99; Mismatches 441; Indels 341; Gaps 47;

Matches 204; Conservative 118; Miatches 441; Indels 341; Gaps 47;

162 FKEAVFMCVFLHYGLDIVHINHGDDTRIPLEPVQLEMPD--VNRLYDPNTNTHFESIG 219

147 FGKLASOLEOLYHENQIET--LDPDSFOHLPKLE-RFLHNNRITHLVPGTN-HLESMK 202

220 EGFTYPTPYNTGCHLHDCYTAPEAYALRVRNVTAVARGAAHLADENHSGAVLPDI 279

Db 203 RLRLDS---NTLHC---DCBTLWADLKLTYAESSNAQAARICEPPR----- 244

Qy 280 TYTFQSSSGTTARGARRNDYNTSKPSPSGGFERLASMADTAFLHAEVTFNTGTY 339

Db 245 ---IQGREGATVTPPEEINCCRRTSEIQ-----DADTSGNTVY 281

Db 246 ---EVKTCBTVLRYFGSP-----ARPTFVIOQPNTEVLGESVT 378

Qy 340 EETPTDIKEWPMPFICMEG-----TLPRLNAL-----GSYTTARVAGYIG 377

Db 282 FTCRAEGNPKEPIWLNNNELSMKTDRNLNUDDGTIMIQNTQETDGIYQCMARNVAG 341

Qy 378 AMVESPNSAVALTEVEDSGMTEAKDGGPSFSNFRFYQAGPHILAANPQTDR-----DGHVL 433

Db 342 -----EVKTCBTVLRYFGSP-----ARPTFVIOQPNTEVLGESVT 378

Qy 434 SSQSTG-----SSSTEFSVDYLALICGCGAPLLARLTYLERCDAGATGGHGD 483

Db 379 ECSAUGHTPPRISNTGDRTPLPYDPRVNITPGSG-----LYIQ-----NVVQGDSSEY 427

Qy 484 LKYYTGTFDSEIPCSLCERKTRPVCAHTVHRLRQRMPEFGQATROPICVFG-TMNSOYS 542

Db 428 ACSATNNIDS-----VHATAPIVYQALQFTVTPQDRVVIEGQTVDFFQ-----470

Qy 543 DCDPILGNYAAYPLILRKPGDQTEAAKATMDTYRATLRLFIDLERLDRGA-PCCSEG 601

Db 471 -CEAKNPPPEVIAINTKGGSQLSV-----DRRHVLLSSSTLRSVGAUHDQGQVEQATN 523

Qy 602 L-SSVIVDHPFTERRDITLARIETCTTQEMKVLYETRDYKIREGLSEATHSMALTEPD 659

Db 524 TIGSQKVAAILTVQPRTPVFAASLPSDT-----VEGANVQLPCCSGEPEPAITWK 577

Qy 660 YSGAFFPITNFLVKRHLAVQDIA-----LSQCHCYFYGQVEGRNF--RNQFQBVLRFF 714

Db 578 DGVQVTESGKPHISPEGLTINDVGPADAGRYEC-----ARNTIGSASVSMVLSYV 630

Db 715 VDLFNGG--F1ST-----RSTVTV-----LSEGPPVSAAPNPTLG-----QDA 748

Qy 631 PDVSRNGDPFTATSIVTATVDRAINSTRTHLDSRSPSPNDLALFYPDQTYVEA 690

Db 746 VNNCSDMCFHQYRTHGTCNNLQHPMWGAISLTAPERLJKSYENGNTFRGINPHRLN 805

Qy 749 PAGRTFDGDLARVSVEVIRDIRVK-----NRVYFGSGNTNLSPRAR 791

Db 691 RAGEITFERTLQIQBTVQHGLMVLDLNGTSYHYNDLVSQYLNIANLSGC-----AHR 745

RESULT 32

US-10-211-462-87

Sequence 87, Application US/10211462

GENERAL INFORMATION: Publication No. US20040033495A1

APPLICANT: Murray, Richard

APPLICANT: Glynn, Richard

APPLICANT: Watson, Susan R.

APPLICANT: Aziz, Natasha

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Angiogenesis, Compositions and Methods of Screening for Angiogenesis Modulators

FILE REFERENCE: 018511-00200US

CURRENT APPLICATION NUMBER: US10/211,462

CURRENT FILING DATE: 2003-02-13

PRIOR APPLICATION NUMBER: US 09/784,356

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: US 09/791,390

PRIOR FILING DATE: 2001-02-22

PRIOR APPLICATION NUMBER: US 60/310,025

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US 60/334,244

PRIOR FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 230

SOFTWARE: Patent-in Ver. 2.1

SEQ ID NO 87

LENGTH: 1495

TYPE: PRT

961 -----SGKPILLPFATGPPTE-----CMRDNESP 984  
 Db 1034 FICPVTPGSSGNRETTISDQ---VRGIIIVSGGAMVOL----AIVATYVRAVGRARQ 1082  
 Qy 985 IPEFLAIDBHRANEQOLGHTSMHTLWFEHNRATTELLKLNPHMDGDTIYXTRKTYGAEIQ 1044  
 Db 1083 HNAFDDWLSLTDEFIARDLBEIH 1106  
 Qy 1045 HITYQHNLKPILGEVGMRTGLEYH 1068

RESULT 33  
 US-10-021-660-125  
 Sequence 125, Application US/10021660  
 Publication No. US20030152926A1  
 GENERAL INFORMATION:  
 APPLICANT: Murray, Richard  
 APPLICANT: Glynne, Richard  
 APPLICANT: Watson, Susan R.  
 APPLICANT: EOS Biotechnology, Inc.  
 TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis, Compositions and Methods of Screening for Angiogenesis  
 TITLE OF INVENTION: Modulators  
 TITLE OF INVENTION: Modulators  
 CURRENT APPLICATION NUMBER: US/10/021,660  
 CURRENT FILING DATE: 2001-12-6  
 PRIOR APPLICATION NUMBER: US/09/784,356  
 PRIOR FILING DATE: 2001-02-14  
 PRIOR APPLICATION NUMBER: US 09/637,977  
 PRIOR FILING DATE: 2000-08-11  
 NUMBER OF SEQ ID NOS: 135  
 SOFTWARE: PaseSeq for Windows Version 3.0  
 SEQ ID NO: 125  
 LENGTH: 1496  
 TYPE: PCT  
 ORGANISM: Homo sapiens  
 US-10-021-660-125

Query Match 1.8%; Score 114.5; DB 14; Length 1496;  
 Best Local Similarity 18.5%; Pred. No. 0.99; Gaps 47;  
 Matches 204; Conservative 118; Mismatches 441; Indels 341;

Qy 162 FKEAVFMCNVFLHYGGLDIVHNGDVTRIPLPVQLMPD--VNRLVPPDNTHRSIG 219  
 Db 147 FKGLASLQEYLHFNQET--LDPDSFQHLKPLE-RLFLHNRITHLPGTEN-HLBSMK 202

Qy 220 EGFTYPTPPYNTGCHLTHCVAPMAYLVRVNTAVARGAAHLAHDENHGAVLPPDI 279  
 Db 203 RLJDS---NTLHC---DCEILWADLILKTYAEGNAQAAICEPRL--- 244

Qy 280 TYTFQSSSSGTARGARRNDYNTSKPSGCGFERRASIMAADTAHLAEIFNTGY 339  
 Db 245 ---IGRSVATIPEELCRPRITSEQ-----DADTSGNTVY 281

Qy 340 BETFDIKWPMFIGMEG----TLPNAL----GSTPARVAVIG 377  
 Db 282 FTCAEGNPPEIWLNNNELSMKTDSSNLLDDGTIMQNTQDGIVYQCMKRNVAG 341

Qy 378 AMVFSPPNSALYLVEDESGMTEAKDGGPSFNRFYQZAGPHLAANPOTDR---DGHVJ 433  
 Db 342 -----EVTKTQETYLRFQSP-----ARPTETIOPNTEVLYGESVTL 378

Qy 434 SSQSTG-----SSNTBEFSYDYLALIGFQAPLLFYLERDGAFTGGHGDAD 483  
 Db 379 ECSATHPPRISWTRGDRTPLPVDPRVNTPSGG-----LYIQ---NVVQGDSEY 427

Qy 484 LKYVGTGFDSIEIPCSUCEXTRPVCAHTTWRFLORMPFFQATPQIGVFG-TMNSOYS 542  
 Db 428 ACSATNIDS-----VHATFITYQALOPTVTFQDRVIEGQTVDFAQ - 470

Qy 543 DCDPLGNYAPYLILRKPGDQTEAKATMQDTYRATLERLFDQRLDGRG-PCSEG 601  
 Db 471 -CEAKGNNPPVIAWTKGSSQLSV-----DRRLVLSSETLRTSGVALHDQGOYECQAVN 523

Qy 602 L--SSSVIYDHPTFERRIDTLRARIETTQFMKVLYVETRDYKIREGLSEATHSMALTEDP 659  
 Db 524 IIGSQKVTAHLTYQPRVTFPASTPSDIT----VEYGANYQOLPCSQGEPEPAITNK 577

Qy 660 YSGAFCPTINFYERTHIAVVAODA---LSQGCHCVFYQQVEGRNF--RNQFDPLVRRF 714  
 Db 578 DGQVYTESKEFHISPEGFLITINDVGPADGRYECV-----ARNTIGASYS/SMVLSYNN 630

Qy 715 VDLFNGG--FIST-----RSITYV--LSEGPVSPAPNPTLG-----ODA 748  
 Db 631 PDVSINGDPFVATIVESAATVDRAINSTRTHLFDSPRSPNLLALERYPRDPTVQ 690

Db 631 RAGEIFERTQLQIQLQHVGHLMDLNGTSYHYNDLVSYQNLNLIANLNGCT----ARR 745

Qy 749 PAGTGDGLARVSVEVDIRYK-----NEVVFSENCTNLSEAABAR 791

Db 792 LVGLDASAYQDQEV-----DMHAGALCFLIKQPHGL-----FPRGMPPN---- 832

Qy 792 LVGLDASAYQDQEV-----DMHAGALCFLIKQPHGL-----FPRGMPPN---- 832

Db 746 VNNCSDMCPEQKVRTHDGTCTNNLQHPMNGASLAFERLJKSYENGFTPGRGPNPHRJYN 805

Qy 833 -----SKSPNPDQWFTWLLQRQNOMPDLTHEETIAAVK--REFEE 872

Db 806 GHALDMPMLVYSTLIGETTYTPBQETHUMQOF----LDHDLDSVTLASQRFSPG 861

Qy 873 YAAINFNLNPPTCI-----GELAQFTYMANJLKYCDHSQMLNTLTSITGA 919

Db 862 QHCSNTVCNSNDPPCSVMPNDNSRARSACRMFFVRS-----SPVCGSGMTSLNNS 913

Qy 920 RRPRDPSVHLWIKFDVTSADITQAKALLEKTEPNLPLWTAFTSTH--LYRAAMNR 977

Db 914 VTPREQINQI-----TSDIASNVYGSTEHARSIRDL-----ASHRGLLRQGIVQR 960

Qy 978 PMVULGISISKYGAAGNNRVRQAGNNWCGNGRNVCPLFTEDTRTRFLIACPR---GG 1033

Db 961 -----SGPLLPFPATGPTE----CMRDNESP 984

Qy 1034 FICPVTPGSSGNRETTISDQ---VRGIIIVSGGAMVQL-----AIYATVVRVAVGRARQ 1082

Db 985 IPCFLAGDHANEQOLGLTSMTLAFREHNRIATELLKLNPHWDGDTIYETRK-VGAEIQ 1044

Qy 1083 HMAFDWWLSLTDDEFARDLBEIH 1106

Db 1045 HITYQHNLKPILGEVGMRTGLEYH 1068

RESULT 34  
 US-10-331-496A-28  
 Sequence 28, Application US/10331496A  
 Publication No. US20030228305A1  
 GENERAL INFORMATION:  
 APPLICANT: FRANTZ, GRETCHEN  
 APPLICANT: HILLIAN, KENNETH J.  
 APPLICANT: PHILLIPS, HEIDI S.  
 APPLICANT: POLACK, PAUL  
 APPLICANT: SMITH, VICTORIA  
 APPLICANT: SPENCER, SUSAN D.  
 APPLICANT: WILLIAMS, P. MICKEY  
 APPLICANT: WU, THOMAS D.  
 APPLICANT: ZHANG, ZEMIN  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
 TREATMENT OF TUMOR  
 FILE REFERENCE: P501481-PCT  
 CURRENT APPLICATION NUMBER: US/10/331,496A  
 CURRENT FILING DATE: 2002-12-30  
 PRIOR APPLICATION NUMBER: US 60/345,444  
 PRIOR FILING DATE: 2002-01-02  
 PRIOR APPLICATION NUMBER: US 60/351,885  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: US 60/360,066  
 PRIOR FILING DATE: 2002-02-15  
 PRIOR APPLICATION NUMBER: US 60/362,004  
 PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US 60/366,869  
 ; PRIOR FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/366,284  
 ; PRIOR FILING DATE: 2002-03-21  
 ; PRIOR APPLICATION NUMBER: US 60/368,679  
 ; PRIOR FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/404,809  
 ; PRIOR FILING DATE: 2002-08-19  
 ; PRIOR APPLICATION NUMBER: US 60/405,645  
 ; PRIOR FILING DATE: 2002-08-21  
 ; SEQ ID NO: 28  
 ; LENGTH: 1496  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-10-331-49A-28

Query Match Score 114.5; DB 15; Length 1496;  
 Best Local Similarity 1.8%;  
 Pred. No. 0.99; Mismatches 411; Indels 341; Gaps 47;  
 Matches 204; Conservative 18.5%;  
 Database: PRIMUS; Application No.: US10276774

Qy 162 FKEAVMCMVFLHYGLDWHNGDVRIPRIPVQLEMPD--VNRLLYDPFNTFHRSIG 219  
 Db 147 FKGLASLQYQYLHNOIE--LQDPSFQLPKLE-RFLHNNRITHLYVGTN-HLESMK 202

Qy 220 EGFTYPTPYNTGQGLHLHDCVAPMAMVALRVENTAVARGAHLADENHGAVLPD1 279  
 Db 203 RLRLDS--NTLHC--DCEBILWLAIDLKTYAEGSNAQAACEFPR--244

Qy 280 TYTYQFQSSSGTTARGARRNDVNSTSKEPSGGFERLASSIMAADTAHAEVNTG1 339  
 Db 245 ---TQGRSYATITPEELNCERPRITSEQ---DADYTSCTNTV 281

Qy 340 BETPDTIKWPMFIGMEG---TLPRINL-----GSTARVAGVIG 377  
 Db 282 FTCAEGNPKPEITWLNNELSMRTDSRNLDDGTLMIQNTOEQDGIYQCMARNAVG 341

Qy 378 AMVFSPPNSALYLTVEEDSGMTAEKGDPGPSPFNRFYQAGPHLAANPQTDR---DGHVL 433  
 Db 342 -----EVXTQETYLRYFGSP-----ARPTFTVQPTONTEVLYGEBSTL 378

Qy 434 SSQSTG-----SSNTFSDYDYLALICGFGAPLLAFYLERCDAGAFTGGHGD1 483  
 Db 379 EC5A1GHPPRISWTRGDTPLPDPERNNTIPSGG-----LYIQ---NIVYQGDCEY 427

Qy 484 LKYYTGTGFDSPICSLCEKHTRPyCAHTVHRQRMPPFGQATRQPFIGVFG-TMNSOY5 542  
 Db 428 ACSATNNIDS-----VHATAPIVQALPPTVTPQDRVIVEGQTVDFQ--470

Qy 543 DCDPGNYAAYPLILRKPGDTEAARATMDTYRATLERFIDQERLDRGA--PCSSBG 601  
 Db 471 -CEAKGNNPPVIAWTKGGSOLSV-----DRHLYLSSGTLRISGVALHDQGQECAWN 523

Qy 602 L--SSVYIVDHPPTERRLDLARARCTTQFMKVLYTETDYK-TREGLSRATHSMALDTP 659  
 Db 524 IIGSOKVVAHTVQPRVTPFASPSDT-----VEGANVOLPCSSSGEPEPATWNK 577

Qy 660 YSGAFCPTINFLVKRTHLAVQDLA--LSQLCHCYPQQVEGRNF--RNOQFQPVLRFF 714  
 Db 578 DGVQTVTESKEPHISPEGELTINDYGPADASRYECY-----ANTIGGASVNVLSTNV 630

Qy 715 VDLFNGS--FIRST-----RSITV--LSGPPVSAFPNPLG-----QD1 748  
 Db 631 PDVSRNGDPPFATSIATVDRAINSTRTHLFDSSRSPNDLIALFRYPRDPTVQCA 690

Qy 749 PAGRTFDGDLARVSVEVDIRVK-----NRVVEGNOTNLSEAAAR 791  
 Db 691 RAGEIFERTLQIQEWHQHGMVNDINGTSHYNDLVSPQYINLNLANSGT----AHR 745

Qy 792 LVGLASAYQREKRV----DMLHGALGFLLKQFQGLL-----FPRGMPPN---832  
 Db 746 VNNCSDMCFCHQYRTHDGTNCNNLQHMMWGAStAFLRLSVEYENGNTPRGINPHRLN 805

Qy 833 -----SKSFNPQWTFWILLORNQMPADKLTHEBTTIAVAK--RETEE 872  
 Db 806 GHALPMPRLVSTTLIGTEVTPBQFTMLMORGQF---LHDLDSTVVALSQARSQDG 861

Qy 873 YAAINFINDPPTCT-----BLLAQYMANLILKYCDHSQQLINTLTSITGA 919  
 Db 862 QHCSNCVCSNDPPPSVMIIPNDSBARSQARCHFVRS-----SPYQGSGCTSLMNS 913

Qy 920 RRPRDPSSVLFWIKDVTSAADIETOQAKALLETEENLPELWTAFTSH--LYRAAMNQR 977  
 Db 914 VYPREQINQ-----TSYTDASNYVGTSHARSIDL----ASHRGILRQGTVQR 960

Qy 978 PMVNLGUSISKYHGAAGNNRVRFORGNWSLNGKNCVNPFLFDRTRFTIACPR---GG 1033

Db 961 -----SGPLPPTGPPT-----CNRDENESP 984

Qy 1034 FICPYTGPSQSGNRETTISDQ---VRGIVSGGAMVQ-----AIYATVVRAGAAQ 1082  
 Db 985 IPCFAGDHRANEQOLGLTSKMTLWFRERNRATLILKCNPHDQDITTYETRKVGAETQ 1044

Qy 1083 HMAFDWLSLTDDFLARDLDEELH 1106  
 Db 1045 HITYQHWLPKLGEYGMRTGEYH 1068

RESULT 35

US-10-276-774-1957  
 ; Sequence 1957, Application US/10276774  
 ; Publication No. US20040053245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; ATTORNEY: Tang, Y, Tom et al  
 ; TITLE OF INVENTION: No. US040053245A1 Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-030  
 ; CURRENT APPLICATION NUMBER: US/10-276-774  
 ; PRIORITY APPLICATION NUMBER: 09/560,875  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIORITY FILING DATE: 2000-04-27  
 ; PRIORITY APPLICATION NUMBER: 09/496,914  
 ; PRIORITY FILING DATE: 2000-02-03  
 ; NUMBER OF SEQ ID NOS: 2700  
 ; SOFTWARE: Custom  
 ; SEQ ID NO: 1957  
 ; LENGTH: 1498  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-276-774-1957

Query Match Score 114.5; DB 12; Length 1498;  
 Best Local Similarity 1.8%;  
 Pred. No. 0.99; Mismatches 41; Indels 341; Gaps 47;  
 Matches 204; Conservative 18.5%;  
 Database: PRIMUS; Application No.: US10276774

Qy 162 FKEAVMCMVFLHYGLDWHNGDVRIPRIPVQLEMPD--VNRLLYDPFNTFHRSIG 219  
 Db 147 FKGLASLQYQYLHNOIE--LQDPSFQLPKLE-RFLHNNRITHLYVGTN-HLESMK 202

Qy 220 EGFTYPTPYNTGQGLHLHDCVAPMAMVALRVENTAVARGAHLADENHGAVLPD1 279  
 Db 203 RLRLDS--NTLHC--DCEBILWLAIDLKTYAEGSNAQAACEFPR--244

Qy 280 TYTYQFQSSSGTTARGARRNDVNSTSKEPSGGFERLASSIMAADTAHAEVNTG1 339  
 Db 245 ---TQGRSYATITPEELNCERPRITSEQ---DADYTSCTNTV 281

Qy 340 BETPDTIKWPMFIGMEG---TLPRINL-----GSTARVAGVIG 377  
 Db 282 FTCAEGNPKPEITWLNNELSMRTDSRNLDDGTLMIQNTOEQDGIYQCMARNAVG 341

Qy 378 AMVFSPPNSALYLTVEEDSGMTAEKGDPGPSPFNRFYQAGPHLAANPQTDR---DGHVL 433  
 Db 342 -----EVXTQETYLRYFGSP-----ARPTFTVQPTONTEVLYGEBSTL 378

Qy 434 SSQSTG-----SSNTFSDYDYLALICGFGAPLLAFYLERCDAGAFTGGHGD1 483  
 Db 379 EC5A1GHPPRISWTRGDTPLPDPERNNTIPSGG-----LYIQ---NIVYQGDCEY 427

Qy 484 LKYYTGTGFDSPICSLCEKHTRPyCAHTVHRQRMPPFGQATRQPFIGVFG-TMNSOY5 542  
 Db 428 ACSATNNIDS-----VHATAPIVQALPPTVTPQDRVIVEGQTVDFQ--470

Qy 543 DCDPGNYAAYPLILRKPGDTEAARATMDTYRATLERFIDQERLDRGA--PCSSBG 601  
 Db 471 -CEAKGNNPPVIAWTKGGSOLSV-----DRHLYLSSGTLRISGVALHDQGQECAWN 523

Qy 602 L--SSVYIVDHPPTERRLDLARARCTTQFMKVLYTETDYK-TREGLSRATHSMALDTP 659  
 Db 524 IIGSOKVVAHTVQPRVTPFASPSDT-----VEGANVOLPCSSSGEPEPATWNK 577

Qy 660 YSGAFCPTINFLVKRTHLAVQDLA--LSQLCHCYPQQVEGRNF--RNOQFQPVLRFF 714  
 Db 578 DGVQTVTESKEPHISPEGELTINDYGPADASRYECY-----ANTIGGASVNVLSTNV 630

Qy 715 VDLFNGS--FIRST-----RSITV--LSGPPVSAFPNPLG-----QD1 748  
 Db 631 PDVSRNGDPPFATSIATVDRAINSTRTHLFDSSRSPNDLIALFRYPRDPTVQCA 690

Qy 749 PAGRTFDGDLARVSVEVDIRVK-----NRVVEGNOTNLSEAAAR 791  
 Db 691 RAGEIFERTLQIQEWHQHGMVNDINGTSHYNDLVSPQYINLNLANSGT----AHR 745

Qy 792 LVGLASAYQREKRV----DMLHGALGFLLKQFQGLL-----FPRGMPPN---832  
 Db 746 VNNCSDMCFCHQYRTHDGTNCNNLQHMMWGAStAFLRLSVEYENGNTPRGINPHRLN 805

Qy 833 -----SKSFNPQWTFWILLORNQMPADKLTHEBTTIAVAK--RETEE 872  
 Db 806 GHALPMPRLVSTTLIGTEVTPBQFTMLMORGQF---LHDLDSTVVALSQARSQDG 861

Qy 873 YAAINFINDPPTCT-----BLLAQYMANLILKYCDHSQQLINTLTSITGA 919  
 Db 862 QHCSNCVCSNDPPPSVMIIPNDSBARSQARCHFVRS-----SPYQGSGCTSLMNS 913

Qy 920 RRPRDPSSVLFWIKDVTSAADIETOQAKALLETEENLPELWTAFTSH--LYRAAMNQR 977  
 Db 914 VYPREQINQ-----TSYTDASNYVGTSHARSIDL----ASHRGILRQGTVQR 960

Qy 978 PMVNLGUSISKYHGAAGNNRVRFORGNWSLNGKNCVNPFLFDRTRFTIACPR---GG 1033

Db 961 -----SGPLPPTGPPT-----CNRDENESP 984

Qy 1034 FICPYTGPSQSGNRETTISDQ---VRGIVSGGAMVQ-----AIYATVVRAGAAQ 1082  
 Db 985 IPCFAGDHRANEQOLGLTSKMTLWFRERNRATLILKCNPHDQDITTYETRKVGAETQ 1044

Qy 1083 HMAFDWLSLTDDFLARDLDEELH 1106  
 Db 1045 HITYQHWLPKLGEYGMRTGEYH 1068

RESULT 35

US-10-276-774-1957  
 ; Sequence 1957, Application US/10276774  
 ; Publication No. US20040053245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; ATTORNEY: Tang, Y, Tom et al  
 ; TITLE OF INVENTION: No. US040053245A1 Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-030  
 ; CURRENT APPLICATION NUMBER: US/10-276-774  
 ; PRIORITY APPLICATION NUMBER: 09/560,875  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIORITY FILING DATE: 2000-04-27  
 ; PRIORITY APPLICATION NUMBER: 09/496,914  
 ; PRIORITY FILING DATE: 2000-02-03  
 ; NUMBER OF SEQ ID NOS: 2700  
 ; SOFTWARE: Custom  
 ; SEQ ID NO: 1957  
 ; LENGTH: 1498  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-276-774-1957

Query Match Score 114.5; DB 12; Length 1498;  
 Best Local Similarity 1.8%;  
 Pred. No. 0.99; Mismatches 41; Indels 341; Gaps 47;  
 Matches 204; Conservative 18.5%;  
 Database: PRIMUS; Application No.: US10276774

Qy 162 FKEAVMCMVFLHYGLDWHNGDVRIPRIPVQLEMPD--VNRLLYDPFNTFHRSIG 219  
 Db 147 FKGLASLQYQYLHNOIE--LQDPSFQLPKLE-RFLHNNRITHLYVGTN-HLESMK 202

Qy 220 EGFTYPTPYNTGQGLHLHDCVAPMAMVALRVENTAVARGAHLADENHGAVLPD1 279  
 Db 203 RLRLDS--NTLHC--DCEBILWLAIDLKTYAEGSNAQAACEFPR--244

Qy 280 TYTYQFQSSSGTTARGARRNDVNSTSKEPSGGFERLASSIMAADTAHAEVNTG1 339  
 Db 245 ---TQGRSYATITPEELNCERPRITSEQ---DADYTSCTNTV 281

Qy 340 BETPDTIKWPMFIGMEG---TLPRINL-----GSTARVAGVIG 377  
 Db 282 FTCAEGNPKPEITWLNNELSMRTDSRNLDDGTLMIQNTOEQDGIYQCMARNAVG 341

Qy 378 AMVFSPPNSALYLTVEEDSGMTAEKGDPGPSPFNRFYQAGPHLAANPQTDR---DGHVL 433  
 Db 342 -----EVXTQETYLRYFGSP-----ARPTFTVQPTONTEVLYGEBSTL 378

Qy 434 SSQSTG-----SSNTFSDYDYLALICGFGAPLLAFYLERCDAGAFTGGHGD1 483  
 Db 379 EC5A1GHPPRISWTRGDTPLPDPERNNTIPSGG-----LYIQ---NIVYQGDCEY 427

Qy 484 LKYYTGTGFDSPICSLCEKHTRPyCAHTVHRQRMPPFGQATRQPFIGVFG-TMNSOY5 542  
 Db 428 ACSATNNIDS-----VHATAPIVQALPPTVTPQDRVIVEGQTVDFQ--470

Qy 543 DCDPGNYAAYPLILRKPGDTEAARATMDTYRATLERFIDQERLDRGA--PCSSBG 601  
 Db 471 -CEAKGNNPPVIAWTKGGSOLSV-----DRHLYLSSGTLRISGVALHDQGQECAWN 523

Qy 602 L--SSVYIVDHPPTERRLDLARARCTTQFMKVLYTETDYK-TREGLSRATHSMALDTP 659  
 Db 524 IIGSOKVVAHTVQPRVTPFASPSDT-----VEGANVOLPCSSSGEPEPATWNK 577

Qy 660 YSGAFCPTINFLVKRTHLAVQDLA--LSQLCHCYPQQVEGRNF--RNOQFQPVLRFF 714  
 Db 578 DGVQTVTESKEPHISPEGELTINDYGPADASRYECY-----ANTIGGASVNVLSTNV 630

Qy 715 VDLFNGS--FIRST-----RSITV--LSGPPVSAFPNPLG-----QD1 748  
 Db 631 PDVSRNGDPPFATSIATVDRAINSTRTHLFDSSRSPNDLIALFRYPRDPTVQCA 690

Qy 749 PAGRTFDGDLARVSVEVDIRVK-----NRVVEGNOTNLSEAAAR 791  
 Db 691 RAGEIFERTLQIQEWHQHGMVNDINGTSHYNDLVSPQYINLNLANSGT----AHR 745

Qy 792 LVGLASAYQREKRV----DMLHGALGFLLKQFQGLL-----FPRGMPPN---832  
 Db 746 VNNCSDMCFCHQYRTHDGTNCNNLQHMMWGAStAFLRLSVEYENGNTPRGINPHRLN 805

Qy 833 -----SKSFNPQWTFWILLORNQMPADKLTHEBTTIAVAK--RETEE 872  
 Db 806 GHALPMPRLVSTTLIGTEVTPBQFTMLMORGQF---LHDLDSTVVALSQARSQDG 861

Qy 873 YAAINFINDPPTCT-----BLLAQYMANLILKYCDHSQQLINTLTSITGA 919  
 Db 862 QHCSNCVCSNDPPPSVMIIPNDSBARSQARCHFVRS-----SPYQGSGCTSLMNS 913

Qy 920 RRPRDPSSVLFWIKDVTSAADIETOQAKALLETEENLPELWTAFTSH--LYRAAMNQR 977  
 Db 914 VYPREQINQ-----TSYTDASNYVGTSHARSIDL----ASHRGILRQGTVQR 960

Qy 978 PMVNLGUSISKYHGAAGNNRVRFORGNWSLNGKNCVNPFLFDRTRFTIACPR---GG 1033

Db 961 -----SGPLPPTGPPT-----CNRDENESP 984

Qy 1034 FICPYTGPSQSGNRETTISDQ---VRGIVSGGAMVQ-----AIYATVVRAGAAQ 1082  
 Db 985 IPCFAGDHRANEQOLGLTSKMTLWFRERNRATLILKCNPHDQDITTYETRKVGAETQ 1044

Qy 1083 HMAFDWLSLTDDFLARDLDEELH 1106  
 Db 1045 HITYQHWLPKLGEYGMRTGEYH 1068

RESULT 35

US-10-276-774-1957  
 ; Sequence 1957, Application US/10276774  
 ; Publication No. US20040053245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; ATTORNEY: Tang, Y, Tom et al  
 ; TITLE OF INVENTION: No. US040053245A1 Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-030  
 ; CURRENT APPLICATION NUMBER: US/10-276-774  
 ; PRIORITY APPLICATION NUMBER: 09/560,875  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIORITY FILING DATE: 2000-04-27  
 ; PRIORITY APPLICATION NUMBER: 09/496,914  
 ; PRIORITY FILING DATE: 2000-02-03  
 ; NUMBER OF SEQ ID NOS: 2700  
 ; SOFTWARE: Custom  
 ; SEQ ID NO: 1957  
 ; LENGTH: 1498  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-276-774-1957

Query Match Score 114.5; DB 12; Length 1498;  
 Best Local Similarity 1.8%;  
 Pred. No. 0.99; Mismatches 41; Indels 341; Gaps 47;  
 Matches 204; Conservative 18.5%;  
 Database: PRIMUS; Application No.: US10276774

Qy 162 FKEAVMCMVFLHYGLDWHNGDVRIPRIPVQLEMPD--VNRLLYDPFNTFHRSIG 219  
 Db 147 FKGLASLQYQYLHNOIE--LQDPSFQLPKLE-RFLHNNRITHLYVGTN-HLESMK 202

Qy 220 EGFTYPTPYNTGQGLHLHDCVAPMAMVALRVENTAVARGAHLADENHGAVLPD1 279  
 Db 203 RLRLDS--NTLHC--DCEBILWLAIDLKTYAEGSNAQAACEFPR--244

Qy 280 TYTYQFQSSSGTTARGARRNDVNSTSKEPSGGFERLASSIMAADTAHAEVNTG1 339  
 Db 245 ---TQGRSYATITPEELNCERPRITSEQ---DADYTSCTNTV 281

Qy 340 BETPDTIKWPMFIGMEG---TLPRINL-----GSTARVAGVIG 377  
 Db 282 FTCAEGNPKPEITWLNNELSMRTDSRNLDDGTLMQNTQETDQGIVQCMARNVAG 341

Qy 378 AMVFSPPNSALYLTVEEDSGMTAEKGDPGPSPFNRFYQAGPHLAANPQTDR---DGHVL 433  
 Db 342 -----EVKIQEVTRVTFYFGSP-----ARPTFVQDNTEVLYGVSVTL 378

Qy 434 SSQSTG-----SSNTFSDYDYLALICGFGAPLLAFYLERCDAGAFTGGHGD1 483

Db 379 EGSATGHPPIRISWTRGDRPLPVDPRVNITPSGG-----LYIQ----NVQGDSGEY 427  
 Qy 484 LKVVTGTFDSIEFPCSLCEKHTRVCANTTIVRLQRNMRFOATROPIGVG-TNNSQYS 542  
 Db 428 ACSATNNIDS-----VHATAPIVQALPQFTVTPQDRVVIEGQTVDQF- 470  
 Qy 543 DCDPLGHYAPYLILRKPGDQTEAAKTMQDVTYRATERLFLDEQRLDGA -PCSSSEG 601  
 Db 471 -CEAIGNPPVIAWTKGSSQLSV-----DRAHHLVLSSTGRISVALHDQYECQAVN 523  
 Qy 602 L--SSVIVDHPPTERRILDTLARIECTTQEMKVLVETRDYKIREGLSEATHSMALTFDF 659  
 Dz 524 IIGSQKTVYAHLYQPRVTFVAFSIPSDIT-----VEVGANYQLPCSQGGBEPALTWNK 577  
 Qy 660 YSGAFCPCPTNFKVTHRHLAVQDIA---LSQCHCVPYQQVEGRNF -RNQFQVLRRRP 714  
 Db 578 DGQVQTESGKFHISPEGFLTINDVGPADAGRYECV-----ARNTIGSAVSMSVLSVNV 630  
 Qy 715 VDLFNGG -FIST-----RSIVFT-----LSEGPPVSAVNPNTLG-----QDA 748  
 Db 631 PDYSRNGDBPVATISIVEAIATVDRAINSTRTHFDSPRSRSPNDLLAFLYPRDPYVEQA 690  
 Qy 749 PAGRTFDGDLARYSVETVDIRYK-----NRVVFSGNCNTLSEARAR 791  
 Db 691 RAGEFERTLQLQEHVQHGLMDLNGTSYHNDLSPQYLNIANSGCT-----AHRR 745  
 Qy 792 LVGLASAYQREQEV-----DMHNGAQLGFLKQFHGL-----FPRGMPPN-----832  
 Db 746 VNNCSDMCFHQKZTHDGTIONLQHPPMGASLTAFERLJKSYENGNTPRGJNPHLYN 805  
 Qy 833 -----SKSPNQFWNTLQRNQMPADLTHEITIAVTK -RFTEE 872  
 Db 806 GHALPMPRLVSTRLTIGERTVTPDQFTMLMONGQF-----LDHDLDSTVVALSQARFSDG 861  
 Qy 873 YAAINFNINLPTCT-----GELAQFYMANLILKCDHSQYLINLTSITGA 919  
 Db 862 QHCSNVCNSNDPPCSVMPPNDRSARSGARCMFVRS-----SPYCGSMTSILMNS 913  
 Qy 920 RRPRDPPSVLHWIRKDVTSAADIEQTQAKALLEKTNPLWLTAAFTSPH -LYRAANQR 977  
 Db 914 VYPREQINQ-----TSYIDAENVYGSTHEARSIRD-----ASHRGLRQGIVQR 960  
 Qy 978 PMVVLGISISKHYGAAGNNRVRQGNWSGUNG3KNCVCPPLFTEDRTRFLIACPR---GG 1033  
 Db 961 -----SGKPLPPATGPTE----CNRDENESP 984  
 Qy 1034 FICPVTGPGSGNRETTLSQ---VRGIIVSGGAMVQ-----AIVATVYRAVGAAQ 1082  
 Db 985 IPCFLAGDHANEOLGLTSMHTLAFREHNRIATEILKLNPHWDGDTIYETRKVGBIQ 1044  
 Qy 1083 HMAFDDBLSLTDDEFIARDDEELH 1106  
 Db 1045 HITYQHWLPKLGEVGMRTLGEYH 1068